

Mellier  
09/784005 Page 1  
Seq. 1D w/  
Interf

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 (c) 1993 - 2000 Compugen Ltd.  
 OM protein - protein search, using SW model  
 Run on : May 24, 2002, 09:46:20 ; Search time 105.62 Seconds  
 (without alignments)  
 26.660 Million cell updates/sec

## ALIGNMENTS

**PRED.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT  
PCT-US00-27741-29  
Sequence 29 Application PCT/US0027741  
; GENERAL INFORMATION:  
; APPLICANT: The Ohio State University Research Foundation  
; TITLE OF INVENTION: Antigenic Modification of Polypeptides  
; FILE REFERENCE: URF 2-056 AVECT  
; CURRENT APPLICATION NUMBER: PCT/US00/27741  
CURRENT FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 09/413, 564  
PRIOR FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: patentIn version 3.0  
SEQ ID NO 29  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(8)  
SEQ ID NO 29  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(8)

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	8	1	PCT-US00-27741-29	Sequence 29, APPL Sequence 2, APPL
2	47	100.0	8	1	PCT-US04-10502-1	Sequence 1, APPL
3	47	100.0	8	1	PCT-US94-10503-1	Sequence 1, APPL
4	47	100.0	8	1	PCT-US96-16603-3	Sequence 3, APPL
5	47	100.0	8	1	PCT-US98-16602-2	Sequence 2, APPL
6	47	100.0	8	3	US-07-721-324-2	Sequence 2, APPL
7	47	100.0	8	3	US-07-721-324-2	Sequence 2, APPL

RESULT 2  
PCT-US01-07479B-2  
; Sequence 2, Application PC/TUS0107479B  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; GURU, ZHONGHONG  
; APPLICANT: TJOENG, FOE SIONG  
; APPLICANT: LI, WEI  
; APPLICANT: MANDRELL, KATHY  
; APPLICANT: LUI, MIN  
APPLICANT: CHEN, NATALIE  
TITLE OF INVENTION: ANTI-HYPERTENSIVE PEPTIDES  
FILE REFERENCE: WTC 6517.1  
CURRENT APPLICATION NUMBER: PCT/TUS01/07479B  
CURRENT FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 60/188,499  
PRIOR FILING DATE: 2000-03-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(8)  
OTHER INFORMATION: Peptide is angiotensin II which is obtained during renin-angiotensin conversion.  
PCT-US01-07479B-2

RESULT 3  
PCT-US94-10502-1  
; Sequence 1, Application PC/TUS9410502  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerrega, Gere S.  
TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS  
TITLE OF INVENTION: THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
; ADDRESS: Robbins, Berliner & Carson  
; STREET: 201 North Figueroa Street, Fifth Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
ZIP: 90012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/TUS94/10503  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-336  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-10502-1

RESULT 4  
PCT-US94-10503-1  
; Sequence 1, Application PC/TUS9410503  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerrega, Gere S.  
TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS  
TITLE OF INVENTION: THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
; ADDRESS: Robbins, Berliner & Carson  
; STREET: 201 North Figueroa Street, Fifth Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
ZIP: 90012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/TUS94/10503  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-336  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-10503-1

RESULT 5  
PCT-US96-16603-3  
; Sequence 3, Application PC/TUS9616603  
; GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER  
 TITLE OF INVENTION: PHOTOSENSITIVE CAGED MACROMOLECULES  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US96/16603  
 FILING DATE: 15-OCT-1996  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/542,927  
 FILING DATE: 13-OCT-1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 0420/055W01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US96-16603-3

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVVYHFP 8  
 QY 1 |||||HFP 8  
 Db 1 DRVVYHFP 8

RESULT 7  
 US-07-721-324-2  
 Sequence 2, Application US07721324  
 GENERAL INFORMATION:  
 APPLICANT: Moor, Graham J.  
 APPLICANT: Habibi, Hamid R.  
 APPLICANT: Matsoukas, John M.  
 TITLE OF INVENTION: Non-dedensitizing Analogs of GnRH and Other Biologically Active Ligands  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Burns, Doane, Swecker & Mathis  
 STREET: 699 Prince Street  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22313-2404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/721,324  
 FILING DATE: 19910701  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Dillahunt, T. G.  
 REGISTRATION NUMBER: 25423  
 REFERENCE/DOCKET NUMBER: 028722-042  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 TELEX: ITT 440 580 BDSM ALE  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US98-15112-2

Query Match 100.0%; Score 47; DB 3; Length 8;  
 US-07-721-324-2

Best Local Similarity 100.0%; Pred. No. 3.2e+06; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
Db 1 DRVYIHPF 8

RESULT 8  
US-07-791-928-8  
; Sequence 8, Application US/07791928  
; GENERAL INFORMATION:  
; APPLICANT: SHOUTZ, JOHN W.  
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,  
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL,  
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100  
; CITY: MILWAUKEE  
; STATE: WISCONSIN  
; COUNTRY: USA  
; ZIP: 53202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,928  
; FILING DATE: 1991112  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SARR, CHARLES S  
; REGISTRATION NUMBER: 30492  
; REFERENCE/DOCKET NUMBER: F.3347-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 255-2022  
; TELEFAX: (608) 255-2182  
; TELEX: 2682 ANDSPARK  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; TOPOLogy: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Binding-site  
; LOCATION: 1  
; OTHER INFORMATION:  
; /label= LABEL  
; /note= "LOCATION OF LISSAMINE RHODAMINE"  
; OTHER INFORMATION: DETECTION TAG  
; US-07-791-928-8

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Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.2e+06; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
Db 1 DRVYIHPF 8

RESULT 10  
US-07-946-062-21  
; Sequence 21, Application US/07946062.  
; GENERAL INFORMATION:  
; APPLICANT: BOODOR, Nicholas  
; TITLE OF INVENTION: BRAIN ENHANCED DELIVERY OF NEUROACTIVE  
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: George Mason Bldg., Washington & Prince Sts.  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/946,062  
; FILING DATE: 17-SEP-1992  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E

RESULT 9  
US-07-906-395-4  
; Sequence 4, Application US/07906395  
; GENERAL INFORMATION:  
; APPLICANT: Hardig, J.W.  
; TITLE OF INVENTION: "Angiotensin IV Peptides and Receptor"  
; NUMBER OF SEQUENCES: 6

REGISTRATION NUMBER: 36,113  
 REFERENCE/DOCKET NUMBER: 038724-055  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1 OTHER INFORMATION: /note= "Position 1 = H-Asp."  
 NAME/KEY: Modified-site  
 LOCATION: 8 OTHER INFORMATION: /note= "Position 8 = Phe-OH."  
 US-07-946-062-21

Query Match Similarity 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Mismatches 0;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

RESULT 11  
 US-08-085-870-3

; Sequence 3, Application US/0808870  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winn, Martin

; APPLICANT: De, Biswanath  
 ; APPLICANT: Zydowsky, Thomas M.  
 ; APPLICANT: Kerkman, Daniel J.  
 ; APPLICANT: DeBernardis, John F.

; APPLICANT: Rosenberg, Saul H.  
 ; APPLICANT: Shiosaki, Kazumi  
 ; APPLICANT: Basna, Fatima Z.  
 ; APPLICANT: Tasker, Andrew S.

; TITLE OF INVENTION: Angiotensin II Receptor Antagonists  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edward H. Gorman, Jr.  
 ; STREET: Abbott Laboratories  
 ; STREET: D-377/RP6D  
 ; STREET: One Abbott Park Road  
 ; CITY: Abbott Park

; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/126,368  
 ; FILING DATE: 12-AUG-2002  
 ; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spitals, John P.  
 ; REGISTRATION NUMBER: 29,215  
 ; REFERENCE/DOCKET NUMBER: 1320-336  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 977-1003  
 ; TELEFAX: (213) 977-1003

; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; TOPOLogy: linear  
 ; MOLECULE TYPE: peptide

US-08-126-368-1

Query Match Similarity 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Mismatches 0;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

RESULT 12  
 US-08-126-368-1

; Sequence 1, Application US/08126368  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rodgers, Kathleen E.

; APPLICANT: dizerrea, Gere S.  
 ; TITLE OF INVENTION: USE OF ANGiotensin III AND ANALOGS  
 ; TITLE OF INVENTION: THEREOF IN TISSUE REPAIR  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Robbins, Berliner & Carson  
 ; STREET: 201 North Figueroa Street, Fifth Floor  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90012

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/126,368  
 ; FILING DATE: 12-AUG-2002  
 ; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spitals, John P.  
 ; REGISTRATION NUMBER: 29,215  
 ; REFERENCE/DOCKET NUMBER: 1320-336  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 977-1003  
 ; TELEFAX: (213) 977-1003

; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; TOPOLogy: linear  
 ; MOLECULE TYPE: peptide

US-08-126-368-1

Query Match Similarity 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Mismatches 0;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

RESULT 13

US-08-126-368A-1

Sequence 1, Application US/08126368A

## GENERAL INFORMATION:

APPLICANT: Rodgers, Kathleen E.

APPLICANT: Diazreca, Gere S.

TITLE OF INVENTION: USE OF ANGiotensin III AND ANALOGS THEREOF IN TISSUE REPAIR

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner &amp; Carson

STREET: 201 North Figueroa Street, Fifth Floor

CITY: Los Angeles

STATE: California

COUNTY: U.S.A.

ZIP: 90012

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08126,368A

FILING DATE:

CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29,215

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 977-1001

TELEFAX: (213) 977-1003

INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-126-368A-1

RESULT 14

US-08-247-451-1

Sequence 1, Application US/08247451

## GENERAL INFORMATION:

APPLICANT: Ananthanarayanan, V. S.

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION AND METHOD

NUMBER OF SEQUENCES: 25

TITLE OF INVENTION: FOR MEDIATING THE PHYSIOLOGICAL EFFECTS OF A COMPOUND

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brody and Neimark

STREET: 419 Seventh St., Suite 300

CITY: Washington, N.W.

STATE: D.C.

COUNTRY: USA

ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,784

FILING DATE: 22 DEC 1994

CLASSIFICATION: 530

## ATTORNEY/AGENT INFORMATION:

NAME: Shelton, Dennis K.

REGISTRATION NUMBER: 26,997

REFERENCE/DOCKET NUMBER: WSUR-1-8113

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 224-0718

TELEFAX: (206) 224-0779

INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

DESCRIPTION: Angiotensin II

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/802,982

FILING DATE: 06-DEC-1991

APPLICATION NUMBER: US 07/323,421

FILING DATE: 14-MAR-1989

## ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANATHANI

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-247-451-1

Query Match

Best Local Similarity 100.0%; Score 47; DB 5; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8

Db 1 DRVYIHPF 8

RESULT 15

US-08-360-784-4

Sequence 4, Application US/08360784

## GENERAL INFORMATION:

APPLICANT: Harding, J.W.

APPLICANT: Wright, J.W.

TITLE OF INVENTION: Angiotensin IV Peptides and Receptor

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

STREET: 1420 Fifth Ave., Suite 2800

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101-2247

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,784

FILING DATE: 22 DEC 1994

CLASSIFICATION: 530

## ATTORNEY/AGENT INFORMATION:

NAME: Shelton, Dennis K.

REGISTRATION NUMBER: 26,997

REFERENCE/DOCKET NUMBER: WSUR-1-8113

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 224-0718

TELEFAX: (206) 224-0779

INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

DESCRIPTION: Angiotensin II

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

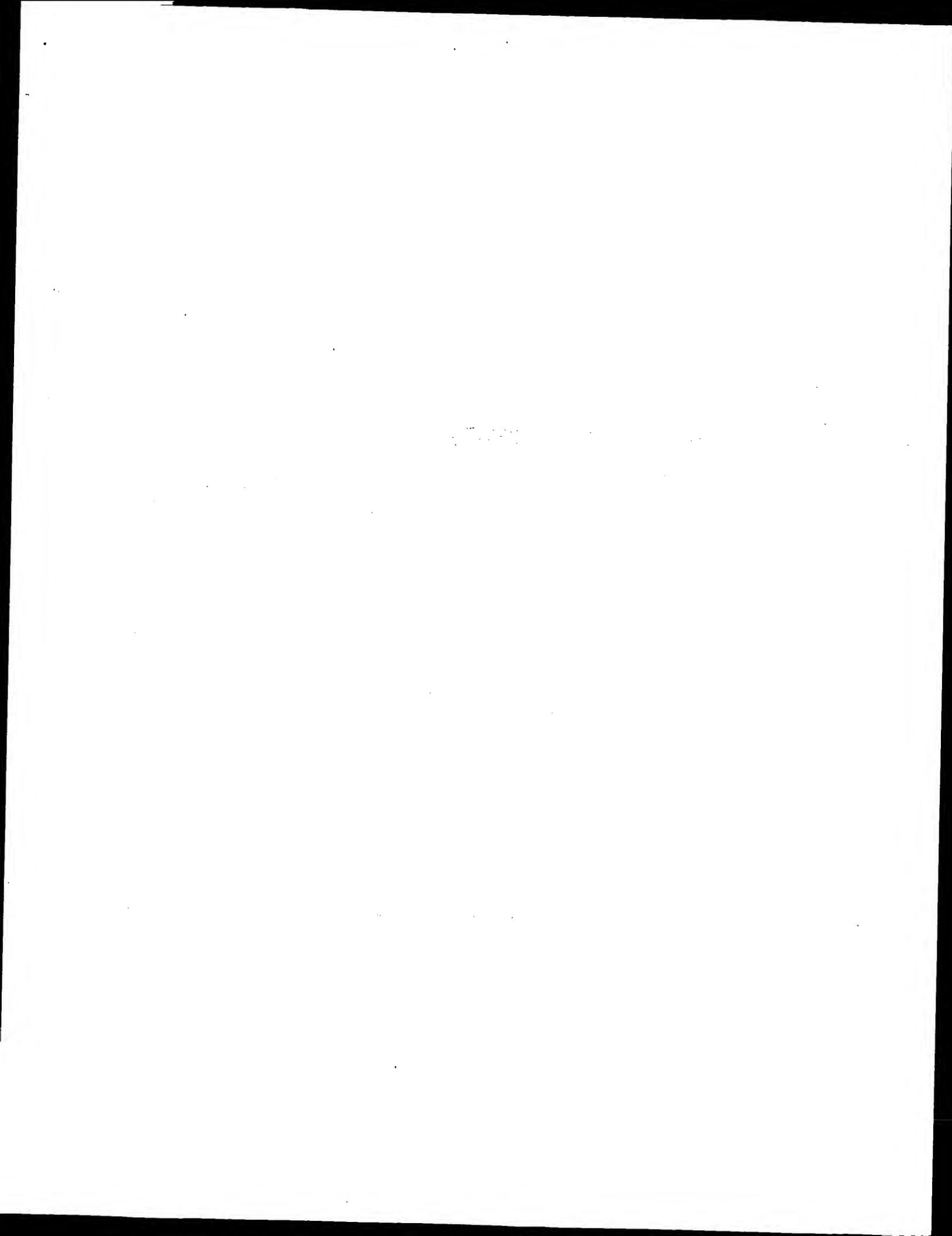
Fri May 24 13:12:20 2002

; ORIGINAL SOURCE:  
; ORGANISM: Bos taurus  
; US-08-360-784-4

Query Match 100.0%; Score 47; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY	1	DRVYIHPF	8
Db	1	DRVYIHPF	8

Search completed: May 24, 2002, 09:49:32  
Job time: 192 sec



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; RESULT 1
; PCT-US02-13383-6
; Sequence 6, Application PC/US0213383
; GENERAL INFORMATION:
; APPLICANT: Tamura, Masaaki
; TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
; FILE REFERENCE: Vanderbilt Ref. No. VU0112; Our Ref. No. 1242-56
; CURRENT APPLICATION NUMBER: PCT/US02/13383
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-13383-6

RESULT 2
US-09-955-780-3
; Sequence 3, Application US/09955780
; GENERAL INFORMATION:
; APPLICANT: Kuo, Gee-Hong
; APPLICANT: Connolly, Peter
; APPLICANT: Proctor, Catherine
; APPLICANT: DeAngelis, Alan
; APPLICANT: Wang, Alhua
; APPLICANT: Jolliffe, Linda
; APPLICANT: Middleton, Steve
; APPLICANT: Emanuel, Stuart
; TITLE OF INVENTION: Pyrazine Derivatives as Modulators of Tyrosine Kinases
; FILE REFERENCE: ORT-1499
; CURRENT APPLICATION NUMBER: US/09/955,780
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/233,968
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8

```



RESULT 7  
 Sequence 32, Application US/09307940B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rodgers, Kathleen  
 ; APPLICANT: dizerega, Gere  
 ; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After  
 ; TITLE OF INVENTION: Chemotherapy  
 ; FILE REFERENCE: 97017P1  
 ; CURRENT APPLICATION NUMBER: US/09/307,940B  
 ; CURRENT FILING DATE: 1999-05-10  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 32  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:ATI analogue 14  
NAME/KEY: MOD\_RES  
LOCATION: (4)  
OTHER INFORMATION: PHOSPHORYLATION  
US-09-307-940B-32

---

Query Match 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHFP 8  
 ; GENERAL INFORMATION:  
 ; APPLICANT: verdine, Greg L.  
 ; APPLICANT: Chytlik, Milan  
 ; APPLICANT: Malinky, Tiffany  
 ; APPLICANT: Didink, Mary T.  
 ; TITLE OF INVENTION: SYNTHESIS OF COMPOUNDS AND LIBRARIES OF  
 ; TITLE OF INVENTION: COMPOUNDS  
FILE REFERENCE: 00246-258001  
CURRENT APPLICATION NUMBER: US/09/273,597  
CURRENT FILING DATE: 1999-03-22  
PRIORITY FILING DATE: 1998-03-23  
NUMBER OF SEQ ID NOS: 7  
SEQ ID NO 7  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-273-597-7

---

RESULT 8  
Sequence 7, Application US/09273597  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Radiation Therapy Methods  
FILE REFERENCE: 97017K4  
CURRENT APPLICATION NUMBER: US/09/716,527  
CURRENT FILING DATE: 2000-11-20  
NUMBER OF SEQ ID NOS: 38  
SEQ ID NO 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:ATI  
US-09-716-527-1

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Query Match 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHFP 8  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rodgers, Kathleen  
 ; APPLICANT: dizerega, Gere  
 ; TITLE OF INVENTION: Radiation Therapy Methods  
FILE REFERENCE: 97017K4  
CURRENT APPLICATION NUMBER: US/09/716,527  
CURRENT FILING DATE: 2000-11-20  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-716-527-1

---

RESULT 11  
Sequence 11, Application US/09608532E  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Use of Anniotensin II Fragments and Analogs Thereof in Tissue  
FILE REFERENCE: USC0101.1C2CCP (00-1188-E)  
CURRENT APPLICATION NUMBER: US/09/608,532E  
CURRENT FILING DATE: 2002-04-24  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: synthetic peptide  
US-09-608-532E-1

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Query Match 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHFP 8  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rodgers, Kathleen  
 ; APPLICANT: dizerega, Gere  
 ; TITLE OF INVENTION: Radiation Therapy Methods  
FILE REFERENCE: 97017K4  
CURRENT APPLICATION NUMBER: US/09/716,527  
CURRENT FILING DATE: 2000-11-20  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AlI analogue 14
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION
; US-09-716-527-32

Query Match      100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DRVVIHPF 8
Db    1 DRVVIHPF 8

RESULT 12
; sequence 1, Application US/09716716
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US-09-716-716
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AlI
; US-09-716-716-1

Query Match      100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DRVVIHPF 8
Db    1 DRVVIHPF 8

RESULT 13
; sequence 32, Application US/09716716
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US/09/716,716
; CURRENT FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AlI analogue 14
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION

Query Match      100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DRVVIHPF 8
Db    1 DRVVIHPF 8

RESULT 14
; sequence 6, Application US/10133056
; GENERAL INFORMATION:
; APPLICANT: Tamura, Masaaki
; TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
; CURRENT APPLICATION NUMBER: US/10/133,056
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-133-056-6

Query Match      100.0%; Score 47; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DRVVIHPF 8
Db    1 DRVVIHPF 8

RESULT 15
; sequence 5, Application PCT/US0213383
; GENERAL INFORMATION:
; APPLICANT: Tamura, Masaaki
; TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
; FILE REFERENCE: Vandebilt Ref. No. VU0112; Our Ref. No. 1242-56
; CURRENT APPLICATION NUMBER: PCT/US02/13383
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-13383-5

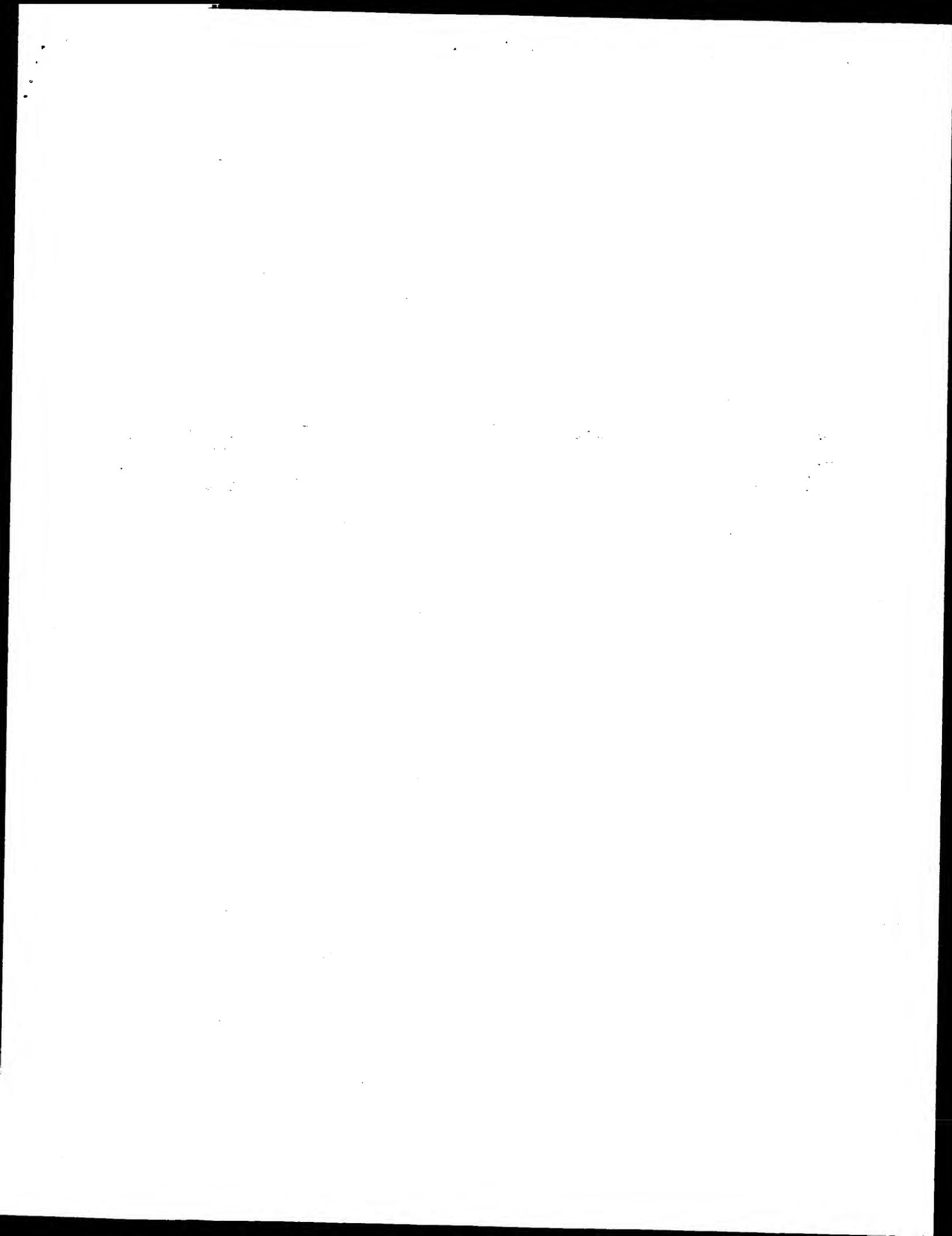
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Search completed: May 24, 2002, 09:49:49
Job time: 209 sec

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Fri May 24 13:12:20 2002

us-09-784-005-1.rapn



Om protein - protein search, using sw model

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Gencore version 4.5

Run on: May 24, 2002, 09:46:20 ; Search time 29.95 seconds  
 (without alignments)  
 29.669 Million cell updates/sec

Title: US-09-784-005-1  
 Perfect score: 47  
 Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 4: /SIDS1/gcadata/hold\_geneseq/geneseqp-emb1/AA1983.DAT: \*  
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 11: /SIDS1/gcadata/hold\_geneseq/geneseqp-emb1/AA1990.DAT: \*  
 12: /SIDS1/gcadata/hold\_geneseq/geneseqp-emb1/AA1991.DAT: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	47	10.0	8	6 AAP50467	Sequence of cyclop
2	47	10.0	8	11 AAR05584	Hypotensive polype
3	47	10.0	8	14 AAR31433	ProMega peptide 8
4	47	10.0	8	15 AAR82013	ProMega protein k1
5	47	10.0	8	16 AAR8269	Angiotensin II dec
6	47	10.0	8	17 AAW65193	Angiotensin II S
7	47	10.0	8	17 AAR95662	Angiotensin II. S
8	47	10.0	8	18 AAW33209	Targetting conjuga
9	47	10.0	8	18 AAW32551	Targetting conjuga
10	47	10.0	8	18 AAW11201	Conjugating peptid
11	47	10.0	8	18 AAW14975	

## SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	47	100.0	8	6	AAP50467	Sequence of cyclop
2	47	100.0	8	11	AAR07584	Hypotensive polype
3	47	100.0	8	14	AAR37433	Promega peptide 8
4	47	100.0	8	16	AAR83013	Promega protein ki
5	47	100.0	8	16	AAR84269	Angiotensin II dec
6	47	100.0	8	17	AAN05193	Angiotensin II. S
7	47	100.0	8	17	AAR05662	Angiotensin II. S
8	47	100.0	8	18	AAN33309	Targetting conjuga
9	47	100.0	8	18	AAN12951	Targetting conjuga
10	47	100.0	8	18	AAN11201	Targetting conjuga
11	47	100.0	8	18	AAN144975	Conjugating peptid

RESULT	1	ALIGNMENTS
AAP50467	( first entry)	
ID	AAP50467 standard; peptide; 8 AA.	
AC	AAP50467;	
XX		
DT	01-DEC-1991	
XX		
DE	Sequence of cyclopropyl peptide with anti-hypertensive activity	
XX		
KW	Cyclopropyl peptide; analgesic; CNS regulator; anti-hypertensive;	
KW	blood pressure regulator; renin inhibitor; anti-hypertensive;	
KW	bradykinin inhibitor; shock therapy.	
XX		
PN	W08500809-A.	
XX		
PD	28-FEB-1985.	
XX		
12	47 100.0	8 18 AAWW9650
13	47 100.0	8 18 AAWW9144
14	47 100.0	8 19 AAWW5595
15	47 100.0	8 19 AAWW4758
16	47 100.0	8 19 AAWW4728
17	47 100.0	8 19 AAWW5628
18	47 100.0	8 19 AAWW1141
19	47 100.0	8 19 AAWW1110
20	47 100.0	8 19 AAWW5538
21	47 100.0	8 19 AAWW9280
22	47 100.0	8 19 AAWW5523
23	47 100.0	8 20 AAYW9586
24	47 100.0	8 20 AYK9614
25	47 100.0	8 20 AAYW9917
26	47 100.0	8 20 AAYW33901
27	47 100.0	8 20 AAYW23679
28	47 100.0	8 20 AAYW3539
29	47 100.0	8 20 AAYW0568
30	47 100.0	8 20 AAYW30583
31	47 100.0	8 20 AAYW36012
32	47 100.0	8 20 AAYW32150
33	47 100.0	8 20 AAYW3743
34	47 100.0	8 20 AAYW3797
35	47 100.0	8 20 AAYW33768
36	47 100.0	8 20 AAYW1573
37	47 100.0	8 20 AAYW13340
38	47 100.0	8 20 AAYW15345
39	47 100.0	8 20 AAYW1533
40	47 100.0	8 20 AAYW21824
41	47 100.0	8 20 AYW94002
42	47 100.0	8 21 AAB27397
43	47 100.0	8 21 AAB27401
44	47 100.0	8 21 AAB27432
45	47 100.0	8 21 AAB28130
46	47 100.0	8 21 AAB28130

XX  
 CC When used to replace normal AAs in a peptide chain, the cyclopropyl  
 CC AAs stabilise the peptide against enzymatic cleavage and acid  
 CC hydrolysis, and the peptide has good long term stability. Peptides  
 CC containing cyclopropyl AAs have numerous pharmacological properties, e.g.  
 CC as bacteriostats, analgesics, CNS regulators, blood pressure regulators, renin inhibitors, antihypertensives and  
 CC bradykinin inhibitors for shock treatment. They may also be  
 CC herbicides, pesticides etc. Dose is 50-100 mg/kg for intravascular  
 CC admin. In AaP50467, optionally the following AAs are cyclopropyl  
 CC residues: 1, 2, 3, 4, 6, 8, 4 and 8, 4 and 6, 6 and 8.  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHPF 8  
 Db 1 ||||||| 1  
 drvyihpf 8  
 RESULT 2  
 AAR07564  
 ID AAR07584 standard; protein; 8 AA.  
 XX  
 AC AAR07584;  
 XX  
 DT 08-FEB-1991 (first entry)  
 XX  
 DE Hypotensive polypeptide.  
 KW Gamma-casein.  
 XX  
 OS Zea mays.  
 XX  
 PN JP02240027-A.  
 XX  
 FD 25-SEP-1990.  
 XX  
 PR 14-MAR-1989; 89JP-0059549.  
 XX  
 PR 14-MAR-1989; 89JP-0059549.  
 XX  
 PA (AGEN ) AGENCY OF IND SCI TECH.  
 PA (SHOS ) SHOWA KK.  
 DR WPI; 1990-332335/44.  
 XX  
 PT New polypeptide hypotensive agents - are tri-, penta- or  
 PT hexapeptide(s) derived from gamma casein  
 XX  
 PS Claim 1; Page 193; 5pp; Japanese.  
 XX  
 CC Peptide, derived from zea mays gamma-casein, is useful as an anti-  
 CC hypertensive agent in mammals and humans.  
 XX  
 SQ Sequence 8 AA;

RESULT 4  
 AAR83013  
 ID AAR83013 standard; peptide; 8 AA.  
 XX  
 AC AAR83013;  
 XX  
 DT 11-APR-1996 (first entry)  
 XX  
 DE Promega protein kinase substrate peptide G.  
 XX  
 KW Promega; peptide; substrate; G; protein kinase; activity; assay.  
 OS Synthetic.

Query Match 100.0%; Score 47; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHPF 8  
 Db 1 ||||||| 1  
 drvyihpf 8  
 RESULT 3  
 AAR37433

PN WO9523612-A1.  
 XX  
 PD 08-SEP-1995.  
 XX  
 PF 06-MAR-1995; 95WO-US02856.  
 PR XX 04-MAR-1994; 94US-0208573.  
 PA (PROM-) PROMEGA CORP.  
 XX  
 PI Goueli SA;  
 XX  
 DR WPI; 1995-320414/41.  
 XX  
 PT Quantitating activity of a selected protein kinase on a peptide substrate - by conjugating the substrate to a binding cpd.  
 XX  
 PS Claim 15; Page 35; 49pp; English.  
 XX  
 CC The activity of a selected protein kinase (PK), pref. Ser-Thr or Tyr PK, is quantified by conjugating a binding cpd. to a peptide substrate, pref. one of the Promega peptides A-H (AAR83007-14), adding this to a PK contg. soln., incubating the soln. to form a modified peptide prod. and then measuring the activity of the PK.  
 CC Sequence 8 AA;  
 SQ

Query Match	Score	DB	Length
Best Local Similarity	100.0%	16	8;
Matches	8;	Prod. No.	6.4e+05;
	Conservative	Indels	0;
	0;	Mismatches	0;
		Gaps	0;

Outer Match 100.0%; Score 47; DB 16; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 drvyihpf 8

RESULT 6  
 AAW65193  
 ID AAW65193 standard; peptide; 8 AA.  
 XX  
 AC AAW65193;  
 XX  
 DT 02-OCT-1998 (first entry)  
 XX  
 DE Angiotensin II.  
 XX  
 KW Bradykinin; N-benzylglycine; agonist; receptor study; antagonist; achiral; analgesic; angiotensin II.  
 XX  
 OS Synthetic.  
 XX  
 PN US55271882-A.  
 XX  
 DD 18-JUN-1996.  
 XX  
 PF 07-NOV-1994; 94US-0335202.  
 XX  
 PR 07-JUL-1989; 89US-0376839.  
 PR 16-SEP-1992; 92US-0945604.  
 PR 07-NOV-1994; 94US-0335202.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Mitchell AR, Young JD;  
 XX  
 DR WPI; 1996-299898730.  
 XX  
 PT New bradykinin analogues contg. N-benzyl-glycine - useful as  
 PT bradykinin agonists or antagonists, useful e.g. as analgesics  
 XX  
 PS Disclosure; Columns 9-10; 15pp; English.  
 XX  
 KW The invention relates to the obtaining of a potent agonist or antagonist  
 XX peptide by the replacement of selected amino acids with synthetic  
 CC achiral amino acids. The present sequence represents angiotensin II  
 CC in which such an amino acid change can be made.  
 XX  
 PN JP07215889-A.  
 XX  
 PD 15-AUG-1995.  
 XX  
 PF 27-JAN-1994; 94JP-0023615.  
 PR XX 27-JAN-1994; 94JP-0023615.  
 PA (SENIN-) SENNI ERESU KK.  
 XX  
 DR WPI; 1995-317421/41.  
 XX  
 PT Hypotensive agent and functional food - composed of angiotensin II  
 PT decomposition peptide  
 XX  
 PS Claim 1; Page 2; 6pp; Japanese.  
 XX  
 CC AAR84268 and AAR84269 are angiotensin II-derived decomposition peptides.  
 CC They are useful as hypotensive agents and may be used in a  
 CC hypothesizing functional food. The peptides show excellent ACE  
 CC inhibiting activity and can be used as effective hypotensive agents.

---

RESULT 5  
 AAR84269  
 ID AAR84269 standard; peptide; 8 AA.  
 XX  
 AC AAR84269;  
 XX  
 DT 11-APR-1996 (first entry)  
 XX  
 DE Angiotensin II decomposition peptide useful as a hypotensive agent.  
 XX  
 KW Angiotensin; hypertension; inhibition; hypotensive functional food;  
 KW ACE; angiotensin converting enzyme.  
 OS Synthetic.  
 XX  
 PN JP07215889-A.  
 XX  
 PD 15-AUG-1995.  
 XX  
 PF 27-JAN-1994; 94JP-0023615.  
 PR XX 27-JAN-1994; 94JP-0023615.  
 PA (SENIN-) SENNI ERESU KK.  
 XX  
 DR WPI; 1995-317421/41.  
 XX  
 PT Hypotensive agent and functional food - composed of angiotensin II  
 PT decomposition peptide  
 XX  
 PS Claim 1; Page 2; 6pp; Japanese.  
 XX  
 CC AAR84268 and AAR84269 are angiotensin II-derived decomposition peptides.  
 CC They are useful as hypotensive agents and may be used in a  
 CC hypothesizing functional food. The peptides show excellent ACE  
 CC inhibiting activity and can be used as effective hypotensive agents.

---

RESULT 7  
 AAR9562  
 ID AAR9562 standard; peptide; 8 AA.  
 XX  
 AC AAR9562;  
 XX  
 DT 09-JAN-1997 (first entry)

DE Angiotensin II.  
 XX KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;  
 KW rhenium; conjugate; endothelin; angiotensin; targetting agent;  
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW delivery.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 PN WO9614858-A1.  
 XX PD 23-MAY-1996.  
 XX PF 14-NOV-1995; 95WO-US14764.  
 XX PR 06-JUN-1995; 95US-0465575.  
 XX PR 14-NOV-1994; 94US-0337781.  
 XX PA (UFRG) UNIV SOUTHERN CALIFORNIA.  
 XX PI Dizerega GS, Rodgers K;  
 PT DR  
 XX WPI: 1996-259561/26.  
 XX PT Accelerating wound healing by application of angiotensin II  
 PT fragments - are effective at very low concn. and do not cause  
 PT hypertension.  
 XX PS Disclosure: Page 2; 46pp; English.  
 CC This sequence represents angiotensin II (AT2). AT2 is an octapeptide  
 CC present in humans and other species. AT2 is one of the most potent  
 CC vasoconstrictors known, causing constriction of the arterioles. The  
 CC formation of angiotensin is initiated by the action of renin on  
 CC angiotensinogen. The substance formed is a decapeptide called  
 CC angiotensin I which is converted by the enzyme angiotensinase (by  
 CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release  
 CC of extracellular matrices involved in wound repair. Fragments of this  
 CC sequence (see AAK5663-R95672) can be used in a compound for  
 CC accelerating wound healing. The compounds are administered as matrical  
 CC or micellar solutions, formulated with a carrier or diluent,  
 CC alternatively the compound is applied in conjunction with a wound  
 CC dressing. The carrier used in the composition is preferably  
 CC carboxymethylcellulose, crystalloids, viscoelastics, or poly glycols. By  
 CC using fragments of this sequence (or analogues of it), growth as well as  
 CC healing of tissues is improved, such as in cases of wounds on the skin  
 CC (e.g. ulcers, burns, periodontal disease, cuts) or intraperitoneal  
 CC surgical wounds. The compounds containing the AT2 fragments are less  
 CC hypertensive than full length AT2, and are also effective at much lower  
 CC concentrations than full length AT2.  
 SQ Sequence 8 AA;  
 RESULT 9  
 ID AAW32951  
 ID AAW32951 standard; peptide; 8 AA.  
 AC AAW32951;  
 XX DT 26-JAN-1998 (first entry)  
 DE Targetting conjugate for bifunctional sulphonamide type ligand.  
 XX KW Bifunctional sulphonamide; ligand; radioactive; technetium;  
 KW rhenium; conjugate; endothelin; angiotensin; targetting agent;  
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW delivery.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 PN DE1953785-A1.  
 XX PD 27-MAR-1997.  
 XX PT  
 XX PF 19-SEP-1996; 96WO-DE01824.  
 XX PR 21-SEP-1995; 95DE-4036783.  
 XX PA (UFRG) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX PI Dinkelborg L, Hilger CS, Kramp W, Platzek J;  
 PT Raduechel B;  
 XX DR WPI: 1997-212562/19.  
 XX PT New bis-nicotinamide bi:functional chelating agents - forming new,  
 PT stable technetium or rhenium complexes and conjugates useful as  
 PT radiodiagnostic and radiotherapeutic agents  
 XX PS Claim 11; Page 42; 47pp; German.  
 CC Novel bis-nicotinamide bi:functional chelating agent for radioactive  
 CC technetium and rhenium, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.  
 XX SQ Sequence 8 AA;  
 Query Match Best Local Similarity 100.0%; Score 47; DB 17; Length 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHPF 8  
 DB 1 DRVYIHPF 8

PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.  
 XX  
 XX Claim 11; Page 18; 19pp; German.  
 PR  
 XX Novel bifunctional sulphonamide type ligands for radioactive  
 PA (UYBE-) UNTV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX technetium and rhenium, when conjugated to an endothelin or  
 PI angiotensin derived targeting agent, e.g. the present peptide, can  
 PT be used for the in vivo imaging of organs, receptors and receptor  
 Raduechel B;  
 XX containing tissues and/or atherosclerotic plaques, e.g. for the  
 DR diagnosis of breast or prostatic carcinoma. They can also be used  
 WPI; 1997-193894/18.  
 XX for cytostatic agent delivery.  
 PT Bifunctional sulphonamide type ligands for radioactive technetium or  
 PT rhenium - and their chelates and conjugates, useful for imaging  
 PT carcinoma or atherosclerosis  
 XX  
 PS Claim 9; Page 11; 12pp; German.  
 XX Novel bifunctional sulphonamide type ligands for radioactive  
 CC technetium and rhenium, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIHPF 8  
 |||||  
 Db 1 drvyihpf 8  
 AC AAWI4975  
 XX  
 RESULT 11  
 AAWI4975 standard; peptide: 8 AA.  
 AC AAWI4975;  
 XX  
 DT 28-NOV-1997 (first entry)  
 DE Conjugating peptide for radio-therapeutic/diagnostic agent.  
 XX  
 KW Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;  
 KW radiodiagnostic; raditherapeutic; diagnosis; tumour; ischaemia;  
 KW atherosclerosis; vascular disorder; ischemia.  
 KW Synthetic.  
 OS  
 XX  
 PN WO9710852-A2.  
 XX  
 PD 27-MAR-1997.  
 XX  
 PP 19-SEP-1996; 96WO-DE01821.  
 XX  
 PR 21-SEP-1995; 95DE-1036785.  
 XX  
 PA (UYBE-) UNTV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 PI Raduechel B;  
 XX DR WPI; 1997-202627/18.  
 XX  
 PT New sulphide-sulphonamide bi-functional chelating agents - forming  
 PT new, stable technetium or rhenium complexes and conjugates useful as  
 PT radiodiagnostic and radio-therapeutic agents  
 XX  
 PS Claim 13; Page 44; 50pp; German.  
 XX  
 CC XNS-type bifunctional sulphide containing sulphonamide chelating  
 CC agents and their technetium or rhenium complexes, can form  
 CC covalently bonded conjugates with substances selectively enriched  
 CC in diseased tissue, e.g. the present peptide. The substance is an  
 CC endothelin or angiotensin peptide, or a partial sequence, analogue,  
 CC derivative or antagonist, or a chemotactic peptide.  
 CC The conjugates are radiodiagnostic or radiotherapeutic agents,  
 CC useful in the diagnosis of tumours, ischaemia or atherosclerotic  
 CC vascular disorders.  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 AC ||||||| 8  
 XX  
 DT 06-AUG-1997 (first entry)  
 XX  
 DE Isoelectric point marker peptide 4 based on angiotensin I.  
 XX  
 KW Label; fluorescent dye; isoelectric; point; PI; marker; focusing;  
 XX  
 OS Synthetic.  
 XX  
 DE Labelled peptide substrate used in enzyme activity assay.  
 XX  
 KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;  
 KW non-radioactive; electrophoretic separation; protein kinase; protease;  
 XX  
 OS Synthetic.  
 XX  
 PH Location/Qualifiers  
 FT Modified-site 1 /note= "labelled with rhodamine B detection tag"  
 XX  
 PN US5580747-A.  
 XX  
 PD 03-DCC-1996.  
 XX  
 PF 12-NOV-1991; 91US-0791928.  
 XX  
 PR 21-JAN-1994; 94US-0185448.  
 XX  
 PR 12-NOV-1991; 91US-0791928.  
 XX  
 PA (PROM-) PROMEGA CORP.  
 XX  
 PT Shultz JW, White DH;  
 XX  
 DR WPI; 1997-001360/01.  
 XX  
 PT Isoelectric point markers for isoelectric focusing - comprising  
 PT fluorescence-labelled oligo:nucleotide(s)  
 XX  
 PS Claim 6; Page 21; 29pp; English.  
 XX  
 CC The present peptide, when labelled with a fluorescent dye, can be  
 CC used as an isoelectric point (PI) marker for isoelectric focusing  
 CC with fluorescence. The dye is linked to the peptide's  
 CC amino-terminal through an amide, thioamide, sulphonamide, urea,  
 CC thione or urethane bond, and is rhodamine, fluorescein, cyanine,  
 CC indocyanine, indocarbocyanine, pyronine, lucifer yellow,  
 CC quinacrine, squarilium, coumarin, fluoroanthranil maleimide or  
 CC anthracene. The marker can be used for capillary isoelectric  
 CC focusing and it is possible to construct peptide sets that cover  
 CC a wide PI range and have good storage stability.  
 CC The present peptide has respective observed and calculated PI  
 CC values of 5.30 and 5.20.  
 XX  
 PS Sequence 8 AA;  
 XX  
 CC Aaw09656 is a peptide substrate used in a non-radioactive assay for  
 CC measuring enzyme activity. The assay comprises incubating the enzyme  
 CC with the labelled peptide substrate to form a labelled peptide  
 product; separating the product from the substrate by agarose gel  
 electrophoresis and measuring the amount of product by detecting the  
 label by fluorescence or chemiluminescence. The assay can be  
 performed rapidly and with great sensitivity. This peptide is  
 especially for determining tyrosine kinase activity, e.g. to study  
 CC its function in metabolism or to screen for potential inhibitors.  
 XX  
 Sequence 8 AA;

---

Query Match 100.0%; Score 47; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 AC ||||||| 8  
 Db 1 dryvihpf 8  
 XX  
 DE Angiotensin II.  
 XX  
 KW angiotensin II; skin graft; All analogue; tissue repair; vasoconstrictor;  
 XX  
 XX

RESULT 13  
 AAW19144  
 ID AAW19144 standard; peptide; 8 AA.  
 XX  
 AC AAW19144;  
 XX  
 DT 06-AUG-1997 (first entry)  
 XX  
 DE Isoelectric point marker peptide 4 based on angiotensin I.  
 XX  
 KW Label; fluorescent dye; isoelectric; point; PI; marker; focusing;  
 XX  
 OS Synthetic.  
 XX  
 PN EP744614-A2.  
 XX  
 PD 27-NOV-1996.  
 XX  
 PR 29-MAR-1996; 96EP-0105113.  
 XX  
 PR 19-OCT-1995; 95JP-0271196.  
 PR 31-MAR-1995; 95JP-0076873.  
 XX  
 PA (MOLE-) LAB MOLECULAR BIOPHOTONICS.  
 XX  
 PI Kasai K, Matsumoto H, Shimura K, Takamoto H;  
 XX  
 DR WPI; 1997-001360/01.  
 XX  
 PT Isoelectric point markers for isoelectric focusing - comprising  
 PT fluorescence-labelled oligo:nucleotide(s)  
 XX  
 PS Claim 6; Page 21; 29pp; English.  
 XX  
 CC The present peptide, when labelled with a fluorescent dye, can be  
 CC used as an isoelectric point (PI) marker for isoelectric focusing  
 CC with fluorescence. The dye is linked to the peptide's  
 CC amino-terminal through an amide, thioamide, sulphonamide, urea,  
 CC thione or urethane bond, and is rhodamine, fluorescein, cyanine,  
 CC indocyanine, indocarbocyanine, pyronine, lucifer yellow,  
 CC quinacrine, squarilium, coumarin, fluoroanthranil maleimide or  
 CC anthracene. The marker can be used for capillary isoelectric  
 CC focusing and it is possible to construct peptide sets that cover  
 CC a wide PI range and have good storage stability.  
 CC The present peptide has respective observed and calculated PI  
 CC values of 5.30 and 5.20.  
 XX  
 PS Sequence 8 AA;  
 XX  
 CC Query Match 100.0%; Score 47; DB 18; Length 8;  
 CC Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 AC AAW65596  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II.  
 XX  
 KW angiotensin II; skin graft; All analogue; tissue repair; vasoconstrictor;  
 XX

RESULT 14  
 AAW65596  
 ID AAW65596 standard; peptide; 8 AA.  
 XX  
 AC AAW65596;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II.  
 XX  
 KW angiotensin II; skin graft; All analogue; tissue repair; vasoconstrictor;  
 XX

OS Homo sapiens.  
 XX WO9826795-A1.  
 PN XX 25-JUN-1998.  
 PD XX PR 16-DEC-1997; 97WO-US23461.  
 PR XX PR 15-DEC-1997; 97US-0990664.  
 PR XX PR 16-DEC-1996; 96US-0028310.  
 PA XX (UWSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PT dizerega GS, Rodgers KE;  
 XX DR WPI; 1998-362518/31.  
 PT XX Promoting incorporation of skin graft onto underlying tissue -  
 PT comprises pre-treating graft with angiotensin II, or analogue or  
 peptide fragment.

XX Claim 1; Page 1; 82PP; English.

PS The invention relates to the use of angiotensin II (AII), AII analogues, All fragments and AII fragment analogues for promoting incorporation of a skin graft into underlying tissue of a mammal. The peptides are effective in accelerating the growth or healing of skin grafts and in accelerating re-epithelialisation and tissue repair, even at very low concentrations. They can significantly accelerate the rate of healing at nanomolar levels in vivo. AII accelerates wound repair by increased neovascularisation, growth factor release, re-epithelialisation, extracellular matrix production and increased flow of blood and nutrients to the injured tissue. Use of the above peptides other than AII itself (an extremely potent vasoconstrictor) may avoid the side-effects of AII, such as increase in blood pressure and thirst. The present sequence represents angiotensin II.

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6 4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 |||||  
 Db 1 dryylhpf 8

---

RESULT 15  
 AAW64758 ID AAW64758 standard; peptide; 8 AA.  
 AC AAW64758;  
 XX DT 02-NOV-1998 (first entry)

DE Angiotensin II peptide analogue 14.

XX Proliferation; mesenchymal stem cell; lineage-specific cell; malignant; KW hematopoietic; cell culture; transplantation; treatment; malignant; inherited disease; angiotensinogen; angiotensin I; angiotensin II.  
 OS Synthetic.  
 OS Homo sapiens.

FH Key Modified-site 4 Location/Qualifiers  
 FT Modified-site 4 /note= "Modified by (P03)2 group"  
 FT XX WO9832457-A2.  
 PN XX PR 30-JUL-1998.

XX PR 26-JAN-1998; 98WO-US01552.  
 XX PR 23-JAN-1998; 98US-0066593.  
 PR 28-JAN-1997; 97US-0036507.  
 PR 08-MAY-1997; 97US-0046859.  
 PR 28-OCT-1997; 97US-0063684.  
 PR 31-OCT-1997; 97US-0063910.  
 PR 18-NOV-1997; 97US-0065612.  
 PR 26-NOV-1997; 97US-0066593.  
 XX PA (UWSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PT dizerega G, Rodgers KE;  
 XX DR WPI; 1998-437044/37.  
 PT XX Promoting haemopoietic and mesenchymal cell proliferation and differentiation - by contacting the cells with angiotensinogen, angiotensin I or II, or analogues or fragments of these.

PS Disclosure; Page 18; 114PP; English.

XX AAW64758-W64763 are peptides used in a novel method for accelerating the proliferation of mesenchymal stem cells (MSCs), haematopoietic lineage-specific cells or mesenchymal lineage-specific cells. The method involves contacting the cells with an active agent comprising a sequence consisting of at least three contiguous amino acids of groups R1-R8 in the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8, R1 and R2 together form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val, Ala, Leu, norleu, Ile, Gly, Pro, Alb, Acpc (1-amino cyclopentane carboxylic acid) or Tyr, R4 = Tyr, R5 = His, Arg or Asp, R6 = Ile, Ala, Leu, norleu, Val or Gly; R6 = His, Arg or Asp, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are not defined in the specification, the peptide bond between Ra and Rb is labile to aminopeptidase A cleavage excluding sequences including R4 as a terminal Tyr group. A second active agent comprising a sequence consisting of at least three contiguous amino acids of groups R7-R8 in the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala, Orn, Ser(AsC), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also described. The inventions are particularly useful in cell culture mediums. These cells may be used in transplantation techniques for treatment of malignant or inherited diseases. The formulae represent analogues of angiotensinogen, angiotensin I (AII), angiotensin II (AII), or AII AT2 type 2 receptor agonists.

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6 4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 |||||  
 Db 1 dryylhpf 8

---

Query Match 100.0%; Score 47; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6 4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 |||||  
 Db 1 dryylhpf 8

Search completed: May 24, 2002, 09:47:40  
 Job time: 80 sec

Fri May 24 13:12:16 2002

us-09-784-005-1.rag

OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 13.03 Seconds  
                   (w/o alignments)  
                   14.997 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Maximum DB seq length: 0

Minimum DB seq length: 0

Post-processing: Minimum Match 0%  
                   Maximum Match 100%  
                   Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /cgn2\_6/ptodata/2/iaa/backfiled.pep:  
 ...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	47	100.0	8	US-07-858-842-2
2	47	100.0	8	Sequence 2, Appl
3	47	100.0	8	Sequence 3, Appl
4	47	100.0	8	Sequence 4, Appl
5	47	100.0	8	Sequence 5, Appl
6	47	100.0	8	Sequence 6, Appl
7	47	100.0	8	Sequence 7, Appl
8	47	100.0	8	Sequence 8, Appl
9	47	100.0	8	Sequence 9, Appl
10	47	100.0	8	Sequence 10, Appl
11	47	100.0	8	Sequence 11, Appl
12	47	100.0	8	Sequence 12, Appl
13	47	100.0	8	Sequence 13, Appl
14	47	100.0	8	Sequence 14, Appl
15	47	100.0	8	Sequence 15, Appl
16	47	100.0	8	Sequence 16, Appl
17	47	100.0	8	Sequence 17, Appl
18	47	100.0	8	Sequence 18, Appl
19	47	100.0	8	Sequence 19, Appl
20	47	100.0	8	Sequence 20, Appl
21	47	100.0	8	Sequence 21, Appl
22	47	100.0	8	Sequence 22, Appl
23	47	100.0	8	Sequence 23, Appl
24	47	100.0	8	Sequence 24, Appl
25	47	100.0	8	Sequence 25, Appl
26	47	100.0	8	Sequence 26, Appl
27	47	100.0	8	Sequence 27, Appl

ALIGNMENTS

---

RESULT 1 US-07-858-842-2

; Sequence 2, Application US/07858842

; Patent No. 5314807

; GENERAL INFORMATION:

;     APPLICANT: Yosikawa, Masaaki

;     APPLICANT: Yokoyama, Keiichi

;     APPLICANT: Hasegawa, Masayasu

;     APPLICANT: Yasumoto, Ryōichi

;     APPLICANT: Fujita, Hiroyuki

;     TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN

;     NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

;     ADDRESSEE: ARMSTRONG & KUBOVICK

;     STREET: 1125 K Street N.W. Suite 1000

;     CITY: Washington

;     STATE: District of Columbia

;     COUNTRY: United States of America

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

;     APPLICATION NUMBER: US/07/858-842

;     FILING DATE: 19920327

;     CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

;     APPLICATION NUMBER: JP 142283

;     FILING DATE: 29 MAR 1991

; PRIORITY APPLICATION DATA:

;     APPLICATION NUMBER: JP 298060

;     FILING DATE: 17-OCT-1991

; ATTORNEY/AGENT INFORMATION:

;     NAME: Gormley, Mary E.

;     REGISTRATION NUMBER: 34, 409

;     REFERENCE/DOCKET NUMBER: 920247

; TELECOMMUNICATION INFORMATION:

;     TELEPHONE: (202) 659-2930

;     TELEFAX: (202) 887-0357

;     TELEX: 440142

; INFORMATION FOR SEQ ID NO: 2:

;     SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-07-858-842-2

Query Match  
Best Local Similarity 100.0%; Score 47; DB 1; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVYIHPF 8  
Db 1 DRYVYIHPF 8

RESULT 2

US-08-021-839A-3  
Sequence 3, Application US/08021839A  
PATENT NO. 5326776

GENERAL INFORMATION:

APPLICANT: Winn, Martin

APPLICANT: De, Biswanath

APPLICANT: Zydcowksy, Thomas M.

APPLICANT: Kerkman, Daniel J.

APPLICANT: Debernardis, John F.

APPLICANT: Rosenberg, Saul H.

APPLICANT: Shiosaki, Kazumi

APPLICANT: Basha, Fatima Z.

APPLICANT: Spina, Kenneth P.

APPLICANT: Von Geldern, Thomas W.

TITLE OF INVENTION: Angiotensin II Receptor Antagonists

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward H. Gorman, Jr.

STREET: Abbott Laboratories

STREET: D-377/AP6D

STREET: One Abbott Park Road

CITY: Abbott Park

STATE: Illinois

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb

COMPUTER: Apple Macintosh IICi

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021, 839A

FILING DATE: 24-FEB-1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/844, 817

FILING DATE: 02-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Steven R. Crowley

REGISTRATION NUMBER: 31, 604

REFERENCE/DOCKET NUMBER: 5136.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 938-7742

TELEFAX: (708) 938-2623

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-021-839A-3

RESULT 3  
US-08-184-935-2  
Sequence 2, Application US/08184935  
PATENT NO. 5476770

GENERAL INFORMATION:

APPLICANT: PRADELLES, PHILIPPE

TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/184, 935

FILING DATE: 24-JAN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5476770man F.

REGISTRATION NUMBER: 24, 618

REFERENCE/DOCKET NUMBER: 846-286-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-2000

TELEFAX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-184-935-2

RESULT 4  
US-08-212-433A-29

Sequence 29, Application US/08212433A

PATENT NO. 553897

GENERAL INFORMATION:

APPLICANT: Yates, III, John R.

TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION

TIME OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart St. Tower

CITY: San Francisco

STATE: CA

Query Match

100.0%; Score 47; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 8; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;



QY 1 DRVYIHPF 8  
 US-08-428-488-21  
 ; sequence 21, Application US/08428488  
 ; Patent No. 5624894  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BODOR, Nicholas S.  
 ; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE  
 ; PEPTIDES BY SEQUENTIAL METABOLISM  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis  
 ; STREET: P.O. Box 1404  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 CURRENT APPLICATION NUMBER: US/08/428,488  
 FILING DATE: 27-APR-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baumelster, Mary Katherine  
 REGISTRATION NUMBER: 26,254  
 REFERENCE/DOCKET NUMBER: 028724-087  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6220  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: Peptide  
 FEATURE: NAME/KEY: Modified-site  
 LOCATION: 1  
 OTHER INFORMATION: /note= "Position 1 = H-Asp."  
 FEATURE: NAME/KEY: Modified-site  
 LOCATION: 8  
 OTHER INFORMATION: /note= "Position 8 = Phe-OH."  
 US-08-428-488-21

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 RESULT 9  
 US-08-240-711-20  
 ; Sequence 20, Application US/08240711  
 ; Patent No. 5679777  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ANDERSON, DAVID C.  
 ; APPLICANT: MATHEWS, ANTHONY J.  
 ; TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brody and Neimark  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/240,711  
 FILING DATE: 12-JUL-1994  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/09713  
 FILING DATE: 06-NOV-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/789,177

QY 1 DRVYIHPF 8  
 US-08-337-781-1  
 ; Sequence 1, Application US/08333781  
 ; Patient No. 5620292  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rodgers, Kathleen E.  
 ; APPLICANT: dizegaga, Gere S.  
 ; TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS

US-08-594-117-1

FILING DATE: 08-NOV-1991  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/7789,179  
 FILING DATE: 08-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COOPER, TIVER P.  
 REGISTRATION NUMBER: 28,005  
 REFERENCE/DOCKET NUMBER: ANDERSON=5A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633

INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-240-711-20

RESULT 11  
 US-08-520-770-2  
 Sequence 2, Application US/08520770

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Sequence 2, Application US/08520770  
 Patent No. 5723307  
 GENERAL INFORMATION:  
 APPLICANT: Tsai, Hsin  
 APPLICANT: Chen, Hui-Ling  
 TITLE OF INVENTION: Fluoroenic Substrates for Assay of  
 TITLE OF INVENTION: Angiotensin Converting Enzyme  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 30-AUG-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LL 1791  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-520-770-2

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

RESULT 10  
 US-08-594-117-1  
 Sequence 1, Application US/08594117

Patent No. 5716935  
 GENERAL INFORMATION:  
 APPLICANT: Rodgers, Kathleen E.  
 APPLICANT: dizega, Gere S.

TITLE OF INVENTION: USE OF ANGIOTENSIN II ANALOGS IN TISSUE  
 TITLE OF INVENTION: REPAIR  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Robbins, Beliner & Carson  
 STREET: 201 No. 5716935th Figueroa Street, Fifth Floor  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90012

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 30-AUG-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LL 1791  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-520-770-2

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8  
 Db 1 DRVYIHPF 8

ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29,215  
 REFERENCE/DOCKET NUMBER: 1920-333  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 977-1001  
 TELEFAX: (213) 977-1003

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

RESULT 12  
 US-08-457-753-20  
 Sequence 20, Application US/08457753  
 Patent No. 5759512  
 GENERAL INFORMATION:  
 APPLICANT: ANDERSON, DAVID C.  
 APPLICANT: MATHEWS, ANTHONY J.  
 TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Brody and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,753  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/240,711  
FILING DATE: 12-JUL-1994  
APPLICATION NUMBER: PCT/US92/09713  
FILING DATE: 06-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/789,177  
FILING DATE: 08-NOV-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/789,179  
FILING DATE: 08-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Tver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON=5A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-457-753-20

Query Match 100.0% Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVIHPF 8  
Db 1 DRYVIHPF 8

RESULT 13

Sequence 1, Application US/08115968

Patent No. 5824696

GENERAL INFORMATION:

APPLICANT: Griswold E., Don

APPLICANT: Wharton, John

TITLE OF INVENTION: Medicaments

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham

STREET: P. O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/115,968

FILING DATE: 01-SEP-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: USC011.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-465-774-1

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Matches	Conservative	0;	Indels	0;	Gaps	0;	
Qy	1	DRVYIHPF	8	100.0%	47	DB 2	Length 8;	8	8;	Conservative	0;	Mismatches	0;	Indels	0;
Db	1	DRVYIHPF	8	100.0%	47	DB 2	Length 8;	8	8;	Conservative	0;	Mismatches	0;	Indels	0;

RESULT 15  
 US-08-360-784B-2  
 ; Sequence 2, Application US/08360784B  
 GENERAL INFORMATION:  
 Patent No. 5854388  
 APPLICANT: Harding, J.W.  
 APPLICANT: Wright, J.W.  
 TITLE OF INVENTION: Angiotensin IV Peptides and Receptor  
 NUMBER OF SEQUENCES: 38  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christensen O'Connor Johnson & Kindness  
 STREET: 1420 Fifth Ave., Suite 2800  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101-2347  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/360,784B  
 FILING DATE: 22-DEC-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sheiness, Diana K.  
 REGISTRATION NUMBER: 35,356  
 REFERENCE/DOCKET NUMBER: WSUR-1-8113  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 224-0735  
 TELEFAX: (206) 224-0779  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 DESCRIPTION: Angiotensin II  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Bos taurus  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: Multiple  
 OTHER INFORMATION:  
 OTHER INFORMATION: /note= Includes variants from which deletions have been made  
 OTHER INFORMATION: at the C-terminus by 1, 2, 3, 4, or 5 residues.  
 US-08-360-784B-2

Query Match 100.0%; score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Mismatches 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8

Fri May 24 13:12:19 2002

us-09-784-005-1.rai

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 14.71 Seconds  
(without alignments)  
52.258 Million cell updates/sec

Title: US-09-784-005-1

Perfct score: 47  
Sequence: DRVYIHPF 8

Scoring table: BLOSUM62  
Gapop 10.0 , gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:  
1: pix1: \*  
2: pix2: \*  
3: pix3: \*  
4: pix4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT	Match	Qy	1 DRVYIHPF 8	Db	1 DRVYIHPF 8
1	47	100.0	10	2 S65432	angiotensin I - horn fly (fragment)	100.0%	Score 47;	DB 2;	Length 10;	
2	47	100.0	14	2 A01250	angiotensin precursor	100.0%	Pred. No. 0.0043;			
3	47	100.0	15	2 A60834	angiotensin precursor	100.0%	Mismatches 0;			
4	47	100.0	476	1 JCC2318	angiotensin precursor	100.0%	Indels 0;			
5	47	100.0	477	1 ANRT	angiotensin precursor	100.0%	Gaps 0;			
6	47	100.0	477	1 A29978	angiotensin precursor	100.0%				
7	47	100.0	485	1 ANHU	angiotensin I - Ja	100.0%				
8	46	97.9	10	2 A60624	angiotensin precursor	97.9%				
9	46	97.9	10	2 A90917	angiotensin precursor	97.9%				
10	46	97.9	10	2 A90345	angiotensin precursor	97.9%				
11	45	95.7	11	2 S07207	angiotensin precursor	95.7%				
12	41	87.2	540	2 S72233	angiotensin precursor	87.2%				
13	40	85.1	128	2 G81220	angiotensin precursor	85.1%				
14	40	85.1	132	2 R82800	angiotensin precursor	85.1%				
15	37	78.7	625	1 TBBO	angiotensin precursor	78.7%				
16	36	76.6	277	2 E86229	angiotensin precursor	76.6%				
17	36	76.6	289	2 C56610	angiotensin precursor	76.6%				
18	36	74.5	167	2 AB2630	angiotensin precursor	74.5%				
19	35	74.5	305	2 D69362	angiotensin precursor	74.5%				
20	35	74.5	1355	1 VEBELL	angiotensin precursor	74.5%				
21	34	72.3	183	1 B95125	angiotensin precursor	72.3%				
22	34	72.3	185	2 F97995	angiotensin precursor	72.3%				
23	34	72.3	316	2 T34838	angiotensin precursor	72.3%				
24	34	72.3	360	1 DMVYLH	angiotensin precursor	72.3%				
25	34	72.3	481	2 S76115	angiotensin precursor	72.3%				
26	34	72.3	510	2 BE4094	angiotensin precursor	72.3%				
27	34	72.3	525	2 G83173	angiotensin precursor	72.3%				
28	34	72.3	736	2 D86271	angiotensin precursor	72.3%				
29			1224	2 T07446	angiotensin precursor					

ALIGMENTS

Query Match Similarity 100.0%; Score 47; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0043; Mismatches 0;  
Matches 8; Conservative 0; Indels 0; Gaps 0;

Query Match Similarity 100.0%; Score 47; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0061; Mismatches 0;  
Matches 8; Conservative 0; Indels 0; Gaps 0;

Query Match Similarity 100.0%; Score 47; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0061; Mismatches 0;  
Matches 8; Conservative 0; Indels 0; Gaps 0;

RESULT 3  
A;60834 angiotensin I precursor - dog (fragment)  
N;Contains: angiotensin I  
N;Alternate names: angiotensinogen I  
C;Species: *Canis lupus familiaris* (dog)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1998  
C;Accession: A60834  
R;Oliver, J.A.  
Hypertension 11, 21-27, 1988  
A;Title: Purification and partial characterization of canine angiotensinogen.  
A;Reference number: A60834; MUID:88113996  
A;Accession: A60834; PIDN:AAA98779.1; PID:g202914  
A;Molecule type: protein  
A;Residues: 1-15 <OL>  
C;Superfamily: antithrombin III  
C;Keywords: antithrombin; plasma  
F;1-10/Product: angiotensin I #status predicted <MAT>  
Query Match 100.0%; Score 47; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred No. 0.0066; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
Qy 1 DRYVIIHFF 8  
Db 1 DRYVIIHFF 8

RESULT 4  
JC2318 angiotensin precursor - sheep  
N;Alternate names: angiotensinogen  
C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)  
C;Accession: JC2318; A01405  
R;Negase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura, R.; Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.; Eur. J. Biochem. 154, 597-601, 1986  
A;Title: purification and characterization of ovine angiotensinogen.  
A;Reference number: JC2318; MUID:95072318  
A;Accession: JC2318  
A;Molecule type: mRNA  
A;Residues: 1-476 <NAG>  
A;Cross-references: DDG:D17520; NID:9575593; PIDN:BAA04470.1; PID:g1197183  
A;Experimental source: liver  
A;Note: the authors translated the codon TTC for residue 465 as Leu  
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.  
A;Title: purification and characterization of ovine angiotensinogen.  
A;Reference number: A25406; MUID:86136099  
A;Accession: A25406  
A;Molecule type: protein  
A;Residues: 25-37, 'X', 39 <PER>  
C;Superfamily: antithrombin III  
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor  
F;25-477/Product: angiotensin I #status predicted <WPT>  
F;25-34/Product: angiotensin II #status experimental <PP1>  
F;25-32/Product: angiotensin III #status experimental <PP2>  
F;26-32/Product: angiotensin II #status experimental <PP3>  
F;295, 319/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 47; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred No. 0.28; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
Qy 1 DRYVIIHFF 8  
Db 25 DRYVIIHFF 32

RESULT 6  
A29978 angiotensin precursor - mouse  
C;Species: *Mus musculus* (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A29978  
R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.  
Genomics 2, 240-248, 1988  
A;Title: Molecular cloning of the mouse angiotensinogen gene.  
A;Reference number: A29978; MUID:88284703  
A;Accession: A29978  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-477 <CLD>  
A;Cross-references: GB:AF045887; GB:J03046; NID:92842773; PIDN:AAC01765.1; PID:g28427  
A;Introns: 27/1; 366/2; 414/3  
C;Superfamily: antithrombin III  
C;Keywords: blood pressure control  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-477/Product: angiotensinogen #status predicted <MAT>  
Query Match 100.0%; Score 47; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred No. 0.28; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
Qy 1 DRYVIIHFF 8  
Db 25 DRYVIIHFF 32

RESULT 5  
ANRT

Db 25 DRVYIHPF 32

RESULT 7

ANNO angiotensin precursor [validated] - human

N;Alternate names: angiotensinogen

N;Contains: angiotensin I; angiotensin II; angiotensin III

C;Species: Homo sapiens (man)

C;Date: 06-Jul-1982 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000

C;Accession: A35203; A31662; I37162; I37169; A60825; I39462; A90487; A90226; I54281; A01

R;Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami, J.; Biol. Chem. 265, 7576-7582, 1990

A;Title: Structure and expression of the human angiotensinogen gene. Identification of a Reference number: A35203; MUID:90237063

A;Accession: A3203

A;Molecule type: DNA

A;Residues: 1-485 <FOUR>

A;Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327

A;Ganillard, I.; Clauser, E.; Corvol, P.

DNA 8, 87-99, 1989

A;Title: Structure of human angiotensinogen gene.

A;Reference number: A31362; MUID:83170129

A;Accession: A31362

A;Molecule type: DNA

A;Residues: 1-267, 'W', 269-332, 'E', 334-485 <GA1>

A;Cross-references: GB:M24686; GB:M24687; GB:M24688

A;Note: the authors translated the codon GAA for residue 333 as Gln

J. Biol. Chem. 269, 28598-28605, 1994

A;Title: Identification of cell type-dependent enhancer core element located in the 3'-dA;Reference number: I37168; MUID:95050659

A;Accession: I37168

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 287-375 <WIB2>

A;Cross-references: EMBL:X15325; NID:928695

R;Kunapuli, S.P.; Benedict, C.R.; Kumar, A.

Arch. Biochem. Biophys. 254, 642-646, 1987

A;Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.

A;Reference number: A60825; MUID:87212053

A;Accession: A60825

A;Molecule type: mRNA

A;Residues: 32-184 <KUN1>

R;Kunapuli, S.P.; Kumar, A.

Circ. Res. 60, 786-790, 1987

A;Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of a Reference number: I39462; MUID:87244745

A;Accession: I39462

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: GB:N69110; NID:9178643; PIDN:AAA52282:1; PID:9553181

A;Cross-references: GB:R02215; NID:9178639; PIDN:AAA51731:1; PID:9178640

A;Note: it is uncertain whether Met-1 or Met-10 is the initiator

R;Teeksbury, D.A.; Dart, R.A.; Travis, J.

Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981

A;Title: The amino terminal amino acid sequence of human angiotensinogen.

A;Reference number: A90226; MUID:81255848

A;Accession: A90226

---

RESULT 8

ANNO angiotensin I - Japanese quail

C;Species: Coturnix coturnix japonica (Japanese quail)

C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999

C;Accession: A60624

R;Takei, Y.; Hasegawa, Y.

Gen. Comp. Endocrinol. 79, 12-22, 1990

A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of t

A;Reference number: A60624; MUID:90284684

A;Accession: A60624

A;Molecule type: protein

A;Residues: 1-10 <TAK>

C;Superfamily: antithrombin III

C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 100.0%; Score 47; DB 1; Length 485;

Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8

Db 34 DRVYIHPF 41

---

RESULT 9

ANNO angiotensin precursor - chicken (fragment)

C;Species: Gallus gallus (chicken)

Query Match 97.9%; Score 46; DB 2; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.0066; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8

Db 1 DRVYIHPF 8

C;ID: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: A90917; A01250  
R; Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2055-2057, 1973  
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its  
A;Reference number: A90917; MJD:7127845  
A;Accession: A90917  
A;Molecule type: protein  
A;Residues: 1-10 <AN1>  
C;Keywords: blood pressure control; hormone; vasoconstrictor  
F;1-10/Product: angiotensin I #status experimental <AN1>  
F;1-8/Product: angiotensin II #status experimental <AN2>

RESULT 12  
S72233 transcription factor tbx6 - mouse  
C.Species: *Mus musculus* (house mouse)  
C.Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C.Accession: S72233; S72232  
R.Aguilin, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.  
submitted to the EMBL Data Library, May 1996  
A.Reference number: S72233  
N:Accession: S72233

```

Query Match      97.9%;   Score 46;   DB 2;   Length 10;
Best Local Similarity 87.5%; Pred. No. 0.0066; Mismatches 0;
Matches 7; Conservative 1; Indels 0; Gaps 0;
Qy          1 DRVVTHPF 8
           ||||:||| 1
Db          1 DRVVYHPP 8

```

A;Biochem: J. 65, 246-254, 1957  
A;Title: The amino acid sequence in a hypertensin.  
A;Reference number: A30345  
A;Accession: Ag0345  
A;Molecule type: protein  
A;Residues: 1-10 <BL2>  
C;Keywords: blood pressure control; hormone; vasoconstrictor  
F1;-10;Product: angiotensin I #status experimental <AN1>  
F1;-8;Product: angiotensin II #status experimental <AN2>

```

Query Match          97.9%; Score 46; DB 2; Length 10;
Best Local Similarity 87.5%; pred. No: 0.0066; 1; Mismatches
Matches 7; Conservative 1; Indels 0; Gaps 0;
Qy      1 DRVYVHDP 8
       ||||.||| 1
Db      1 DRVYVHDP 8

```

**RESULT** 11

S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C.Species: Crinia georgiana

C.Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Aug-2000

C.Accession: S07207

R.Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Eidean, R.

C:Species: Crinia georgiana  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Aug-2000  
C:Accession: S07207  
R:Author: Braspern, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.  
R:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1  
R:Reference number: S07207; MUID:80024575  
R:Accession: S07207  
A:Molecule type: protein  
A:Residues: 1-11 <ERS>  
A:Superfamily: unassigned animal peptides  
A:Family: unassigned animal peptides

Query Match 95.7%; Score 45; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 0.011; Mismatches 0; Indels  
 Matches 6; Conservative 2;  
 DRYVYHPP 8  
 |||:|||  
 DRYVHPP 11

A; Reference number: A81000; MUID:20175755  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-128 <TET>  
 A; Cross References: GB:AE002382; GB:AE002098; NID:97225470; PIDN:AAF40714.1; PID:9722  
 A; Experimental source: serogroup B, strain MC58  
 C; GenBank:  
 A; Gene: NMB0260  
 C; Superfamily: Neisseria meningitidis hypothetical protein NMB0260  
 Query Match 85.1%; Score 40; DB 2; Length 128;  
 Best Local Similarity 62.5%; Pred. NO. 1.5;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0.

## RESULT 14

FR2800

hypothetical protein XF0493 [imported] - *Xylella fastidiosa* (strain 9a5c)C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C;Accession: FR2800

C;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequer

C;Nature: 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:2036517

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: FR2800

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 &lt;SIM&gt;

A;Cross-references: GB:AE003898; GB:AE003849; PIDN:AAF83303.1; GSPDB:GN001

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Astruda, P.; Abravanel, R.; Alvaranga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.F.A.; Carraro, D.M.; Carrer, H

as Neto, E.; Docena, C.; El-Dorry, H.; Facineani, A.P.; Ferreira, A.J.S.

R;submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Froehm

A;J.D.; Junqueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laird

J.D.; M.A.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, F

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tsuhako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

A;Genes: XF0493

A;Note: disulfide bonds and carbohydrate binding sites were determined

R;Park, C.H.; Tulinsky, A.

Biochemistry 25, 3977-3982, 1986

A;Title: Three-dimensional structure of the kringle sequence: structure of prothrombi

A;Reference number: A37553; MUID:8629631

A;Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms

R;Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A.

Biochemistry 24, 6854-6861, 1985

A;Title: Characterization of the bovine prothrombin gene.

A;Reference number: A37554; MUID:86077733

A;Contents: annotation; gene structure

R;MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980

A;Title: Cloning and analysis of a cDNA coding for bovine prothrombin.

A;Reference number: I46045; MUID:81054926

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Accession: I46045

A;Molecule Type: mRNA

A;Residues: 466-599, N, 601-625 &lt;MA2&gt;

A;Cross-references: EMBL:V00135; PIDN:9772; PIDN:CAA23451.1; PID:9808945

R;Deijer, G.; Karlstrom, A.R.; Berg, L.

Eur. J. Biochem. 227, 102-107, 1995

A;Title: Identification of the proteolytic thrombin fragments formed after cleavage w

A;Reference number: S67518; MUID:95154277

A;Accession: S67518

A;Status: preliminary

A;Molecule type: protein

A;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; g1

C;Comment: The prothrombin precursor is synthesized in the liver.

C;Superfamily: thrombin; gla domain homology

C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombin

C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb

C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi

C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi

tivation peptide and cleaves the remaining part into light and heavy chains. The acti

C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb

C;Comment: The prothrombin precursor is synthesized in the liver.

C;Comment: The prothrombin precursor is synthesized in the liver.

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C;Comment: The prothrombin precursor is synthesized in the liver.

C;Comment: The prothrombin precursor is synthesized in the liver.

C;Comment: The prothrombin precursor is synthesized in the liver.

Query Match

Best Local Similarity

Score

40;

DB

2;

Length

132;

Matches

5;

Conservative

3;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37;

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

71.4%

DB

2;

Length

601;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

78.7%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

44.1%

DB

984;

Length

132;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match

Best Local Similarity

Score

37.0%

DB

1;

Length

625;

Matches

5;

Conservative

2;

Mismatches

0;

Indels

0;

Fri May 24 13:12:21 2002

us-09-784-005-1.rpr

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2002, 09:47:05 ; Search time 10.37 Seconds  
(without alignments)  
29.870 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47  
Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Swissprot:40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	47	100.0	8	ANG2_BOTJA
2	47	100.0	14	ANGT_HORSE
3	47	100.0	476	ANGT_SHEEP
4	47	100.0	477	ANGT_RAT
5	47	100.0	477	ANGT_MOUSE
6	47	100.0	485	ANGT_HUMAN
7	46	97.9	10	ANGT_BOVIN
8	46	97.9	10	ANGT_CHICK
9	46	95.7	11	ANGT_CRIGE
10	41	87.2	436	TBKA_HUMAN
11	41	87.2	540	TRBX6_MOUSE
12	41	87.2	625	THRB_BOVIN
13	37	78.7	1	ENDL_ARCFU
14	35	74.5	305	TX18_HUMAN
15	35	74.5	501	TX15_MOUSE
16	35	74.5	602	TX11_MOUSE
17	35	74.5	613	VKG46_HS7V
18	35	74.5	1355	SDHD_YEAST
19	34	72.3	360	1_V335_SYN3
20	34	72.3	481	Y335_SYN3
21	34	72.3	1	GDA_PSEAE
22	34	72.3	1224	REPQ_PINTH
23	34	72.3	3110	1_IMA2_HUMAN
24	33	70.2	1	BPH_BOVIN
25	33	70.2	332	GALE_STRTR
26	33	70.2	333	1_GALE_STRTU
27	33	70.2	422	TRBL_BACSU
28	33	70.2	465	Y093_RHIME
29	33	70.2	510	PKG1_PSESM
30	33	70.2	528	GD_DROME
31	33	70.2	617	1_TURB_RAT
32	33	70.2	622	1_THRB_HUMAN
33	70.2		1	TRBL_MOUSE

RESULT	1	ANGL_BOTJA	STANDARD;	PRT;	8 AA.
ID	ANGL_BOTJA				
AC	Q10582;				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	Angiotensin-like peptide II (Fragment).				
DR	Bothrops jararaca (Jararaca); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC	Viperidae; Crotalinae; Bothrops;				
OX	NEBLITaxID=8724;				
[1]					
RP	SEQUENCE;				
RC	TISSUE;Plasma;				
RX	MEDLINE;96208932; PubMed=8829801;				
RA	Borghesani R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;				
RT	"Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca"; Comp. Biochem. Physiol. 113B:467-473(1996).				
CC	-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.				
DR	INTERPRO: IPR002115; SERPIN.				
PROSITE: PS00284; SERPIN; PARTIAL.					
KW	Vasoconstrictor; Plasma; Serpin.				
FT	NON_TER 8 8				
SQ	SEQUENCE				
Query	Match	100.0%;	Score 47;	DB 1;	Length 8;
Matches	8	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DRVYIHPF 8			
Db	1	DRVYIHPF 8			
RESULT	2				
ID	ANGT_HORSE	STANDARD;	PRT;	14 AA.	
AC	P01016;				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	21-JUL-1986	(Rel. 40, Last annotation update)			
DE	Angiotensinogen [contains: Angiotensin I; Angiotensin II] (Fragment).				
GN	SERPINAB OR AGT.				
OS	Equis caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus;				
OX	NCBL-TaxID=9796;				
RN	[1]				
RP	SEQUENCE;				
RA	Skeegs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;				
RT	"The preparation, purification, and amino acid sequence of a polypeptide renin substrate.";				
RT	Q64336 mus musculus				
RT	Q16650 homo sapien				
RT	P15156 mesocricetus				
RT	P03606 caenorhabditis				
RT	P25394 bacillus su				
RT	Q92295 mus musculus				
RT	O9167 homo sapien				
RT	P03442 thermus aqu				
RT	Q83419 treponema p				
RT	Q03077 entamoeba h				
RT	P39173 escherichia				
RT	Q6293 methanobacter				
RT	Q9395 c hexapreny				

RJ J. EXP Med. 106:439-453(1957).  
 CC FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINogen. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A01250; A01250.  
 DR InterPro; IPR000227; Angiotensnsgn.  
 DR Pfam; PF00079; serpin; I.  
 DR PRINS; PR00554; ANGIOENSNGN.  
 DR SMART; SM00093; SERPIN; I.  
 DR PROSITE; PS00384; SERPIN; I.  
 KW Vasconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL  
 FT CHAIN  
 FT PEPTIDE 25 476 ANGIOTENSIN II.  
 FT PEPTIDE 25 32 ANGIOTENSIN I.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;  
 SQ

Query Match 100.0%; Score 47; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;  
 Qy 1 DRYVTHPF 8  
 Do 1 DRYVTHPF 8

RESULT 3  
 ANGT\_SHEEP STANDARD; PRT; 476 AA.  
 ID ANGT\_SHEEP  
 AC P20757;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
 GN SERPINB8 OR AGT.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1] SEQUENCE FROM N.A.  
 RB TISSUE=Liver;  
 RX MEDLINE=95072318; PubMed=7765514;  
 RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,  
 RA Murakami K., Nakamura Y.;  
 RT "Sequencing and expression of sheep angiotensinogen cDNA."  
 RL Biotechol. Biotechnol. 58:1884-1885(1994).  
 RN [2] SEQUENCE OF 25-39.  
 RX MEDLINE=86136059; PubMed=3081342;  
 RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;  
 RT "Purification and characterization of ovine angiotensinogen."  
 RL J. Biochem. 154:591-601(1986).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINogen. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to licensee@isb-sib.ch).  
 CC  
 DR EMBL; D17520; BAA04470.1; -.  
 DR PIR; A25006; A25406.  
 DR InterPro; IPR000227; Angiotensnsgn.  
 DR Pfam; PF00079; serpin; I.  
 DR PRINS; PR00554; ANGIOENSNGN.  
 DR SMART; SM00093; SERPIN; I.  
 DR PROSITE; PS00384; SERPIN; I.  
 KW Vasconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL  
 FT CHAIN  
 FT PEPTIDE 25 476 ANGIOTENSIN II.  
 FT PEPTIDE 25 32 ANGIOTENSIN I.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;  
 SQ

Query Match 100.0%; Score 47; DB 1; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;  
 Qy 1 DRYVTHPF 8  
 Do 25 DRYVTHPF 32

RESULT 4  
 ANGT\_MOUSE STANDARD; PRT; 477 AA.  
 ID ANGT\_MOUSE  
 AC P11859;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
 GN SERPINB8 OR AGT.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE=88284703; PubMed=3397061;  
 RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;  
 RT "Molecular cloning of the mouse angiotensinogen gene.",  
 RL Genomics 2:240-248(1998).  
 CC  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINogen. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
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 CC or send an email to licensee@isb-sib.ch).  
 CC  
 DR EMBL; AF045887; AAC01765.1; -.  
 DR EMBL; AF045886; AAC01765.1; JOINED.  
 DR EMBL; AF045885; AAC01765.1; JOINED.  
 DR EMBL; AF045884; AAC01765.1; JOINED.  
 DR PIR; A29976; A29978.  
 DR MGI; 87963; Aqt.  
 DR InterPro; IPR000227; Angiotensnsgn.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; I.  
 DR PRINTS; PR00654; ANGIOENSNGN.  
 DR SMART; SM00093; SERPIN; I.

DR PROSTINE; PS00284; SERPIN; FALSE NEG.  
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 477 ANGIOTENSINOGEN.  
 FT PEPTIDE 25 34 ANGIOTENSIN I.  
 FT PEPTIDE 25 32 ANGIOTENSIN II.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 477 AA; 51991 MW; A87F4029F38607 CRC64;  
 SQ SEQUENCE 477 AA; 51991 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; RT

Qy 1 DRVYIHPF 8  
 Db 25 DRVYIHPF 32

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RESULT 5  
 ID ANGT\_RAT  
 ID ANGT\_RAT STANDARD; PRT; 477 AA.  
 AC P01015;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin III].  
 GN SERPINA8 OR AGT.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR;  
 RX MEDLINE=83169849; PubMed=6572971;  
 RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S., Nakajima S.;  
 RA "Comparative studies on angiotensins. II. Structure of rat angiotensin and its identification by DNS-method.";  
 RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).  
 RN [2]  
 RP SEQUENCE OF 25-34.  
 RX MEDLINE=73060322; PubMed=4344907;  
 RA Nakayama T., Nakajima T., Sodek H.;  
 RA "Cloning and sequence analysis of cDNA for rat angiotensinogen. II. Structure of rat angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 20:1579-1581(1972).  
 RT - FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
 CC -1 TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR EMBL; 100094; AAA98779.1;  
 DR EMBL; 100091; AAA98779.1; JOINED.  
 DR EMBL; 100092; AAA98779.1; JOINED.  
 DR EMBL; 100093; AAA98779.1; JOINED.  
 PIR; A01251; ANRT.  
 InterPro; IPR000227; Angiotensinogen.  
 DR InterPro; IPR000215; Serpin.

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DR Pfam; PF00079; serpin; 1.  
 DR PRINTS; PR0054; ANGIOTENSIN.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSTINE; PS00284; SERPIN; FALSE NEG.  
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL 1 24 ANGIOTENSINOGEN.  
 FT CHAIN 25 477 ANGIOTENSIN I.  
 FT PEPTIDE 25 34 ANGIOTENSIN II.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 477 AA; 51991 MW; A87F4029F38607 CRC64;  
 SQ SEQUENCE 477 AA; 51991 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; RT

Qy 1 DRVYIHPF 8  
 Db 25 DRVYIHPF 32

---

RESULT 6  
 ID ANGT\_HUMAN  
 ID ANGT\_HUMAN STANDARD; PRT; 485 AA.  
 AC P01019; Q16358; Q16359;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin III].  
 DE SERPINA8 OR AGT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89170129; PubMed=2924688;  
 RA Gaillard I., Clauser E., Corvol P.;  
 RA "Structure of human angiotensinogen gene.";  
 RL DNA 8-87-99(1989);  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85000425; PubMed=6089875;  
 RA Kageyama R., Ohkubo H., Nakajishi S.;  
 RA "Primary structure of human preangiotensinogen deduced from the cloned cDNA sequence.";  
 RL Biochemistry 23:3603-3609(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90237063; PubMed=1692023;  
 RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S., Murakami K.;  
 RA "Structure and expression of the human angiotensinogen gene. Identification of a unique and highly active promoter.";  
 RL J. Biol. Chem. 265:5756-5762(1990).  
 RN [4]  
 RP SEQUENCE OF 1-338 FROM N.A.  
 RX MEDLINE=8724474; PubMed=2885106;  
 RA Kunapuli S.P., Kumar A.;  
 RA "Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.";  
 RL Circ. Res. 60:786-790(1987).  
 RN [5]  
 RP SEQUENCE OF 34-45, AND SUBUNITS.  
 RC TISSUE-Serum;  
 RX MEDLINE=9529395a; PubMed=7539791;  
 RA Oxyng C., Haaning J., Kristensen L., Wagner J.M., Rubin I., Stigbrand T., Gleicher G.J., Sottrup-Jensen L.;  
 RT "Identification of angiotensinogen and complement C3g as novel proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma.";

J. Biol. Chem. 270:13645-13651(1995).  
 DR EMBL; S78530; AAD14288.1; -.  
 RN DR PIR; A01249; ANHU.  
 SEQUENCE OF 34-43.  
 RP DR PIR; A31362; A31362.  
 RX DR A33203; A35203.  
 RA DR SWISS-2DPAGE; P01019; HUMAN.  
 RL DR MIM; 105150; -.  
 RL DR InterPro; IPR00227; Angiotensn.  
 RN DR InterPro; IPR000215; serpin.  
 RP DR PIR0079; serpin; I.  
 RX DR PRINTS; PRO0654; ANGIOESENSGN.  
 RA DR SMART; SM0093; SERPIN; 1.  
 RT DR PROSITE; PS00284; SERPIN; 1.  
 RL KW Vasocostrictor; Glycoprotein; Plasma; Serpin; Signal;  
 RN KW Disease mutation; Polymorphism.  
 RP FT SIGNAL 1 33  
 RX FT CHAIN 34 485 ANGIOTENSINOGEN.  
 RA FT PEPTIDE 34 43 ANGIOTENSIN I.  
 RA FT CARBOHD 47 47 ANGIOTENSIN II.  
 RA FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 RT FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 RL FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 RN FT VARIANT 207 207 T -> M.  
 RX FT FTId=VAR\_007093.  
 RA FT T -> I (IN HYPERTENSION).  
 RA FT /FTId=VAR\_007094.  
 RA FT L -> R (IN HYPERTENSION).  
 RA FT /FTId=VAR\_007095.  
 RT FT M -> T (IN HYPERTENSION).  
 RN FT /FTId=VAR\_007096.  
 RN FT Y -> C (IN HYPERTENSION).  
 RP FT /FTId=VAR\_007097.  
 CC FT VARIANT 281 281 /> E (IN REF. 1).  
 CC FT CONFLICT 333 333 0 -> E (IN REF. 1).  
 RA FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD236E CRC64;  
 RT RN [1]  
 RT RN "detection and characterization of new mutations in the human  
 angiotensinogen gene (AGT);"  
 RT RN Hum. Genet. 96:110-112(1995).  
 RT RN -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN, ACE (ANGIOTENSIN  
 CC CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC CC BALANCE OF BODY FLUIDS.  
 CC CC -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2  
 CC CC heterotetramer with the pro-PRG2 and c3dg  
 CC CC a 2:2 heterohexamer (PIH) (PRECLAMPSTA).  
 CC CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC CC -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
 CC CC ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
 CC CC (PIH) (PRECLAMPSTA).  
 CC CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
 CC CC  
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 CC CC -----  
 DR EMBL; K02215; AA51731.1; -  
 DR EMBL; M24689; AA51590.1; -  
 DR EMBL; M24686; AA51679.1; JOINED.  
 DR EMBL; M24687; AA51679.1; JOINED.  
 DR EMBL; M24688; AA51679.1; JOINED.  
 DR EMBL; X15324; CAA33385.1; -  
 DR EMBL; X15325; CAA33385.1; JOINED.  
 DR EMBL; X15326; CAA33385.1; JOINED.  
 DR EMBL; X15327; CAA33385.1; JOINED.  
 DR EMBL; M69110; AA512282.1; -  
 DR EMBL; S78529; AAD14287.1; -  
 DR EMBL; K02215; AA51731.1; -  
 DR EMBL; M24689; AA51590.1; -  
 DR EMBL; M24686; AA51679.1; JOINED.  
 DR EMBL; M24687; AA51679.1; JOINED.  
 DR EMBL; M24688; AA51679.1; JOINED.  
 DR EMBL; X15324; CAA33385.1; -  
 DR EMBL; X15325; CAA33385.1; JOINED.  
 DR EMBL; X15326; CAA33385.1; JOINED.  
 DR EMBL; X15327; CAA33385.1; JOINED.  
 DR EMBL; M69110; AA512282.1; -  
 DR EMBL; S78529; AAD14287.1; -

RESULT 7  
 ANGL-BOTJA STANDARD; PRT; 10 AA.  
 ID ANGL-BOTJA  
 AC 010581;  
 DT 01-Oct-1995 (Rel. 34, Created)  
 DR 01-Oct-1996 (Rel. 34, Last sequence update)  
 DT 15-Dec-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;  
 OC Lepiosauria; Squamata; Scelopoglossa; Serpentes; Colubroidea;  
 OC Viperidae; Croalinae; Bothrops.  
 RN NCBI-TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208332; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucce J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RL plasma of the snake Bothrops jararaca"; Comp. Biochem. Physiol. 113B:467-473 (1996).  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR00215; serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;



Matches	6; Conservative	2; Mismatches	0; Indels	0; Gaps	0;
OY	1 DRVYIHPF 8				
Db	4 DRVYIHPF 11				
RESULT	11				
TBX6_HUMAN					
ID TBX6_HUMAN	STANDARD;	PRT;	436 AA.		
AC 09547;					
DT 15-JUL-1999 (Rel. 38, Created)					
DT 15-JUL-1999 (Rel. 38, Last sequence update)					
DT 01-MAR-2002 (Rel. 41, Last annotation update)					
DE T-box transcription factor TBX6 (T-box protein 6).					
GN TBX6.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
OC NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=99134303; PubMed=9933572;					
RA Papaietrov C., Putt W., Fox M., Edwards Y.H., "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";					
RL Genomics 55:238-241(1999).					
RN [2]					
RP SEQUENCE OF 135-272 FROM N.A.					
RC TISSUE=Myeloid;					
RX MEDLINE=99107806; PubMed=988994;					
RA Armstrong J.A., Li Q.-Y., Ellington K., Pachham E.A., "Identification, mapping and phylogenomic analysis of four new human members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";					
RL Genomics 55:10-20(1999).					
-!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).					
-!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).					
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).					
-!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL, BUD, POSTERIOR SPINAL TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.					
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A SECOND PHASE IN SOME ADULT TISSUES.					
-!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.					
-----					
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CC -----					
DR RESULT 12					
DR TBX6_MOUSE	STANDARD;	PRT;	540 AA.		
DR ID TBX6_MOUSE					
DR AC P0327;					
DR DT 01-NOV-1997 (Rel. 35, Created)					
DR DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DR DT 01-MAR-2002 (Rel. 41, Last annotation update)					
DR DE T-box transcription factor TBX6 (T-box protein 6).					
DR GN TBX6.					
DR OS Mus musculus (Mouse).					
DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
DR OC NCBI_TaxID=10090;					
DR RN [1]					
DR RP SEQUENCE FROM N.A.					
DR RC TISSUE=Embryo;					
DR RX MEDLINE=97032942; PubMed=8878690;					
DR RP SEQUENCE FROM N.A.					
DR RC TISSUE=Gastrula;					
DR RX MEDLINE=97151702; PubMed=8954725;					
DR RA Chapman D.I., Aquilnik I., Hancock S., Silver L.M., Papaiconnou V.E., "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at gastrulation," Dev. Biol. 180:534-542(1996).					
DR RT Dev. Biol. 180:534-542(1996).					
DR RL [3]					
DR RP FUNCTION.					
DR RX MEDLINE=99140705; PubMed=9490412;					
DR RA Chapman D.I., Papaiconnou V.E., "Three neural T-Box genes with mutations in the T-box gene Tbx6.", Nature 391:695-697(1998).					
DR RT Nature 391:695-697(1998).					
DR RL [4]					
DR CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL PATHWAY.					
DR CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).					
DR CC -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESMOTIC PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK AS THE SOURCE OF MESODERM.					
DR CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.					
DR CC -----					
DR CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/CC">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).					
DR CC -----					
DR DR EMBL U07331; AAC53110.1; -.					
DR DR HSSP; P24781; IXB.R.					
DR DR MGD; MG1:102539; Tbx6.					
DR DR InterPro; IPR006699; T-box.					
DR DR PRINTS; PR00937; TBOX.					
DR DR PRINTS; PR00937; TBOX.					
FT DNA_BIND 100 273 T-BOX.					
FT CONFLICT 207 207 H -> HV (IN REF. 2)					
SQ SEQUENCE 436 AA; 47017 MW; 438178BB31B966E9 CRC64;					

DR SMART; SM00425; TBXO; 1;  
 DR PROSITE; PS01283; TBXO\_1; 1.  
 DR PROSITE; PS01284; TBXO\_2; 1.  
 DR PROSITE; PS50252; TBXO\_3; 1.  
 KW transcription regulation; DNA-binding; Nuclear protein;  
 KW developmental protein.  
 FT DOMAIN 61 64  
 FT DOMAIN 79 82  
 FT DNA\_BIND 100 273  
 SQ SEQUENCE 540 AA; 58628 MW; BC834CE2745E8E61 CRC64;

Query Match 87.2%; Score 41; DB 1; Length 540;  
 Best local similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

OY 1 DRYVIIHP 7  
 |||||  
 Db 170 DRYVIIHP 176

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RESULT 13

ID THRB\_BOVIN STANDARD: PRT; 625 AA.

AC P00735;  
 AC 21-JUL-1986 (Rel. 01, 'Created')  
 DT 01-APR-1990 (Rel. 14, 'Last sequence update')  
 DT 16-OCT-2001 (Rel. 40, 'Last annotation update')  
 DE Prothrombin precursor (EC 3.4.21.5).  
 GN F2.  
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBL\_TAXID=9913;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RN MEDLINE=81245190; PubMed=3379642;  
 RX MEDLINE=84203525; PubMed=6326605;  
 RA Irwin D.M., Robertson K.A.; McGillivray R.T.A.;  
 RT "Structure and evolution of the bovine prothrombin gene.;"  
 RL J. Mol. Biol. 200:31-45(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84203525; PubMed=6326605;  
 RA McGillivray R.T.A.; Davie E.W.;  
 RT "Characterization of bovine prothrombin mRNA and its translation  
 product."  
 RL Biochemistry 23:1626-1634(1984).  
 RN [3]  
 RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
 RA Magnusson S., Sottrup-Jensen L., Peterson T.E., Claeyns H.;  
 RL (In) Henkem H.C., Veitcamp J.J. (eds.);  
 RL Boerhaave symposium on prothrombin and related coagulation factors,  
 RL Biochemistry 23:1626-1634(1984).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX MEDLINE=86296631; PubMed=3741841;  
 RA Park C.H., Tulinsky A.;  
 RT "Three-dimensional structure of the kringle sequence: structure of  
 prothrombin fragment 1.;"  
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A  
 resolution."  
 RL Biochemistry 25:3977-3982(1996).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX MEDLINE=91311686; PubMed=1056869;  
 RA Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;  
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A  
 resolution."  
 RL J. Mol. Biol. 220:481-494(1991).

RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
 RX MEDLINE=92190185; PubMed=1547238;  
 RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;  
 RT "The Ca<sup>2+</sup> ion and membrane binding structure of the Gla domain of Ca-

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RT prothrombin fragment 1.";  
 RL Biochemistry 31:2554-2566(1992).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=9218459; PubMed=1560020;  
 RA Martin P.D., Robertson K.A., Turk D., Huber R., Bode W., Edwards B.F.P.;  
 RT "The structure of residues 7-16 of the A alpha-chain of human  
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";  
 RL J. Biol. Chem. 267:7911-7920(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=92389319; PubMed=1518046;  
 RA Brandstetter H., Turk D., Hoffken H.W., Grossé D., Stuerzebecher J.,  
 RA Martin P.D., Edwards B.F.P., Bode W.;  
 RT "Refined 2.3 A X-ray crystal structure of bovine thrombin inhibitors  
 formed with the benzamidine and arginine-based thrombin  
 NAPAP, 4-TAPAP and MOPA. A starting point for improving  
 RT antithrombotics";  
 RT J. Mol. Biol. 226:1085-1089(1992).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.  
 RX MEDLINE=97102783; PubMed=8947023;  
 RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bolischweiler C.,  
 RA Hoffken W., Huber R.;  
 RT "The ornithodorin-thrombin crystal structure, a key to the TAP  
 RT enigma?";  
 RL EMBO J. 15:6011-6017(1996).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.  
 RX MEDLINE=98004486; PubMed=3342325;  
 RA Fuentes-Prior P., Noeske Jungblut C., Donner P., Schleuning W.D.,  
 RA Huber R., Bode W.;  
 RT "Structure of the thrombin complex with triabin, a lipocalin-like  
 RT exosite-binding inhibitor derived from a triatomine bug.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).  
 RN [11]  
 RP GENE STRUCTURE.  
 RX MEDLINE=86077733; PubMed=3000440;  
 RA Irwin D.M., Alvern K.G.; Pearson G.D., McGillivray R.T.A.;  
 RT "Characterization of the bovine prothrombin gene.";  
 RL Biochemistry 24:6844-6851(1985).  
 CC -1- FUNCTION: THROMBIN WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS  
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,  
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.  
 CC -1- SUBCELLULAR LOCATION: extracellular.  
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.  
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,  
 CC RESULT FROM THE CARBOXYGLUTAMYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL  
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES  
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY  
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION  
 CC OF PROTHROMBIN TO THROMBIN.  
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A  
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF ROTHROMBIN &  
 CC FACTORS VA & VA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES  
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &  
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR  
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF  
 CC THROMBIN.  
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL  
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION  
 CC BY FACTOR XA.  
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 CC -1- DATABASE: NAME-Prozyme technical fact sheet;  
 CC WWW="http://www.prozyme.com/technical/thrombindata.html".  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC	MOD-RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID.
CC	MOD-RES	73	73	GAMMA-CARBOXYGLUTAMIC ACID.
DR	MOD-RES	76	76	GAMMA-CARBOXYGLUTAMIC ACID.
DR	CARBOHYD	120	120	N-LINKED (GLCNAC. . .).
PIR; S02537; S02337.				
PDB; 1BBR; 31-JAN-94.				
PDB; 1EIR; 31-JAN-94.				
DR	PDB; 1EWS; 31-JAN-94.			
DR	PDB; 1ETT; 31-JAN-94.			
DR	PDB; 1HRT; 31-JAN-94.			
DR	PDB; 2BFI; 31-JAN-94.			
DR	PDB; 2BPP2; 31-JAN-94.			
DR	PDB; 2BPT; 31-MAY-94.			
DR	PDB; 1MKW; 07-JULY-97.			
DR	PDB; 1MKX; 07-JULY-97.			
DR	PDB; 1VCP; 06-MAY-98.			
DR	PDB; 1A0H; 17-JUN-98.			
DR	PDB; 1AVG; 16-FEB-99.			
DR	MEROPS; S01_217; -			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR002383; GLA_blood.			
DR	InterPro; IPR000001; Kringle <sup>2</sup> .			
DR	InterPro; IPR003956; Prothrombin.			
DR	InterPro; IPR001254; trypsin.			
DR	InterPro; IPR000294; VitK_dpp_GLA.			
DR	Pfam; PF00594; gta; 1.			
DR	Pfam; PF00551; kringle; 2.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PRINTS; PR00001; GLABLOOD.			
DR	PRINTS; PR0018; KRINGLE.			
DR	PRINTS; PR01505; PROTHROMBIN.			
DR	SMART; SMN00130; KR; 2.			
DR	SMART; SMN0020; TRYSP; 1.			
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.			
DR	PROSITE; PS00021; KRINGLE_1; 2.			
DR	PROSITE; PS00070; KRINGLE_2; 2.			
DR	PROSITE; PS00240; TRIPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRIPSIN_HIS; 1.			
KW	Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Hydrolyase; Serine protease; Kringle; Signal; 3D-structure.			
FT	SIGNAL; 1	24	POTENTIAL.	
FT	PROPEP	25	43	
FT	CHAIN	44	625	PROTHROMBIN.
FT	PEPTIDE	44	199	ACTIVATION PEPTIDE (FRAGMENT 1).
FT	PEPTIDE	200	317	ACTIVATION PEPTIDE (FRAGMENT 1).
FT	CHAIN	318	366	ACTIVATION PEPTIDE (FRAGMENT 2).
FT	CHAIN	367	625	THROMBIN LIGHT CHAIN (A).
FT	DOMAIN	109	187	THROMBIN HEAVY CHAIN (B).
FT	DOMAIN	214	292	KRINGLE 1.
FT	DOMAIN	367	625	KRINGLE 2.
FT	SITE	199	200	SERINE PROTEASE.
FT	SITE	317	318	CLEAVAGE (BY THROMBIN).
FT	SITE	366	367	CLEAVAGE (BY FACTOR XA).
FT	ACT_SITE	409	409	CLEAVAGE (BY FACTOR XA).
FT	ACT_SITE	465	465	CHARGE RELAY SYSTEM.
FT	ACT_SITE	571	571	CHARGE RELAY SYSTEM.
FT	MOD_RES	50	50	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	51	51	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	58	58	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	63	63	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	64	64	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	69	69	GAMMA-CARBOXYGLUTAMIC ACID.

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Query Match	Best Local Similarity	Score	DB	Length
Qy 1 DRVYIHP 7	71.4%	37	1	625;
Db 448 DKIVIHP 454	71.4%	37	12	0;
OC	Indels	0	0	0;
OC	Gaps	0	0	0;
OS	Matches	5	2	0;
OC	Mismatches	0	0	0;
OC	DB	0	0	0;
OC	Score	35	DB 1;	Length 305;
OC	Query Match	74.5%	DB 1;	Length 305;

RESULTS 14

FT	MOD-RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD-RES	73	73	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD-RES	76	76	GAMMA-CARBOXYGLUTAMIC ACID.
FT	CARBOHYD	120	120	N-LINKED (GLCNAC. . .).
DR	ENDA_ARCFU			
DR	ENDA_ARCFU			
AC	029302;			
DT	15-DEC-1998 (Rel. 37, created)			
DT	15-DEC-1998 (Rel. 37, last sequence update)			
DE	PUTATIVE INTRON ENDONUCLEASE (EC 3.1.27.9).			
GN	ENDA OR AF0900			
RA	Archaeoglobus fulgidus.			
RA	Archaeoglobales; Archaeoglobaceae;			
RA	Archaeoglobus			
OX	NCBI_TAXID2234;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VC-16 / DSM 4304 / ATCC 49550;			
RX	MEDLINE-9809343; Published=389475;			
RA	Kleinj. H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,			
RA	Ketchum K.A., Dodson R.J., Gwin M., Hickey E.K., Peterson J.D.,			
RA	Richardson D.L., Kerlavage A.R., Graham D.E., Korpides N.C.,			
RA	Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,			
RA	Peterson S., Reich C.I., McNeil L.K., Badger A.J., Glodek A., Zhou L.,			
RA	Overbeek R., Goedae J.D., Weidman J.F., McDonald L., Utterback T.,			
RA	Cotton M.D., Arpaiges T., Artiach P., Kaine B.P., Sykes S.M.,			
RA	Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,			
RA	Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,			
RA	Venter J.C.,			
RT	"The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."			
RL	Nature 390:364-370(1997).			
CC	RELEASE THE INTRON. THE PRODUCTS ARE AN INTRON AND TWO tRNA HALF-MOLECULES BEARING 2', 3' CYCLIC PHOSPHATE AND 5'-OH TERMINI (BY SIMILARITY).			
CC	-!- FUNCTION: CLEAVES PRE-tRNA AT THE 5' AND 3' SPLICE SITES TO PROTHROMBIN.			
CC	producing 5'-hydroxyl and 2', 3'-cyclic phosphate termini, and SPECIFICALLY REMOVING THE INTRON.			
CC	-!- SIMILARITY: BELONGS TO THE tRNA INTRON ENDONUCLEASE FAMILY.			
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CC	EMBL; AF000141; AAB9038.1; -			
DR	HSSP; 058819; 1479.			
DR	TIGR; AF0900; -			
DR	InterPro; IPR002427; tRNA_int_endo.			
DR	Pfam; PF01974; tRNA_int_endo.			
DR	Pfam; PF02778; tRNA_int_endo.1.			
DR	Hydrolease; Nuclease; Endonuclease; tRNA processing; complete proteome.			
SQ	SEQUENCE 305 AA; 35959 MW; DC0B5A5DEBD9E35 CRC64;			

Query Match 74.5%; Score 35; DB 1; Length 305;

Best Local Similarity 57.1%; Pred. No. 14;保守性 3; Mismatches 4;

Matches 4; Conservative 3; Mismatches 0;

Search completed: May 24, 2002, 09:50:38  
Job time: 213 sec

QY 1 DRVYIHP 7  
|:|:||  
Db 26 DKIYLHP 32

RESULT 15

TX18\_HUMAN STANDARD: PRT; 501 AA.

ID TX18\_HUMAN STANDARD: PRT; 501 AA.

AC 095935; Q9UJ16;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE T-box transcription factor TBX18 (T-box protein 18) (Fragment).

GN TBX18

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID:9606;

RN [1]

SEQUENCE FROM N.A.

RA Bates K.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

RL [2]

RP SEQUENCE OF 42-223 FROM N.A.

RX MEDLINE=99107806; PUBMED=9888994;

RA YI C.-H., Terrett J.A., Li O.-Y., Ellington K., Packham E.A.,

RT Armstrong-Buisseret L., McCue P., Slingsby T., Brock J.D.;

RT "Identification, mapping and phylogenomic analysis of four new human

members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19.";

RL Genomics 55:10-20(1999).

CC FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN

CC DEVELOPMENTAL PROCESSES.

CC --> SOURCELOCATION: Nuclear (Potential).

CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN

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CC -----

Query Match 74.5%; Score 35; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 23; Mismatches 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RVYIHP 7  
|:|:||

Db 115 RVYIHP 120

Fri May 24 13:12:21 2002

us-09-784-005-1.rsp

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**OM protein - protein search, using sw model.**

**Run on:** May 24, 2002, 09:46:45 ; Search time 25.12 Seconds  
(without alignments) updates/sec 55.094 Million cell

**Title:** US-09-784-005-1  
**Perfect score:** 47  
**Sequence:** 1 DRYVIHPF 8

**Scoring table:** BLOSUM62  
Gapopen 10.0 , Gapext 0.5

**Searched:** 562222 seqs, 172991929 residues

**Total number of hits satisfying chosen parameters:** 562222

**Minimum DB seq length:** 0

**Maximum DB seq length:** 200000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

- 1: SPTREMBL\_19;\*
- 2: sp\_archea;\*
- 3: sp\_bacteria;\*
- 4: sp\_fungi;\*
- 5: sp\_invertebrate;\*
- 6: sp\_mammal;\*
- 7: sp\_mhc;\*
- 8: sp\_organelle;\*
- 9: sp\_phage;\*
- 10: sp\_plant;\*
- 11: sp Rodent;\*
- 12: sp\_virus;\*
- 13: sp\_vertebrate;\*
- 14: sp\_unclassified;\*
- 15: sp\_rvirus;\*
- 16: sp\_bacteriaph;\*
- 17: sp\_archeap;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	47	100.0	14	5 Q10757
2	47	100.0	245	6 Q95J13
3	47	100.0	461	11 Q9D2V0
4	47	100.0	477	4 Q9EFD5
5	47	100.0	485	6 Q9GP7
6	47	100.0	485	6 Q9GLP6
7	47	100.0	485	6 Q9G1P6
8	47	100.0	485	6 Q9G1N8
9	47	100.0	486	6 Q9TSZQ
10	46	97.9	13	Q9PS07
11	41	87.2	295	4 Q9H44
12	40	85.1	128	16 Q9KIA7
13	40	85.1	132	16 Q9PG09
14	38	80.9	171	17 Q971G2
15	37	78.7	168	8 Q48244
16	37	78.7	168	8 Q48245

**ALIGNMENTS**

RESULT	ID	PRELIMINARY;	PRT;	14 AA.
1	Q10757	Q10757	Q10757	AC
				DT 01-NOV-1996 (TREMBUREL_01, Created)
				DT 01-NOV-1996 (TREMBUREL_01, Last sequence update)
				DT 01-NOV-1998 (TREMBUREL_08, Last annotation update)
				DR ANGIOTENSINONE (FRAGMENT)
				OS Theryomyzon tessulatum (Leech).
				OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
				OC Rhynchobdellida; Glossiphoniidae; Theryomyzon.
				OC NCBI_TaxID=13286;
				RN [1]
				RN SEQUENCE.
				RX MEDLINE=93365039; PubMed=7637887;
				RA Laurent V.; Bullet P.; Salzet M.A.;
				"A comparison of the leech Theryomyzon tessulatum angiotensins: a hormonal system molecule with forms of vertebrate angiotensinogens conserved in the course of evolution.";
				RT Neurosci. Lett. 190:175-178(1995).
				RN [2]
				RN SEQUENCE OF 1-10.
				RC TISSUE-BRAIN;
				RX MEDLINE=96201949; PubMed=8612806;
				RA Laurent V.; Salzet M.;
				"Metabolism of angiotensins by head membranes of the leech Theryomyzon tessulatum.";
				RL FEBS Lett. 384:123-127(1996).
				CC "FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS."
				KW Glycoprotein; Serpin.
				FT NON_TER 14
				SEQUENCE 14 AA; 1763 MN; 335109D8EEFBDD7 CRC64;
				QY 1 DRYVIHPF 8

Query Match 100.0%; Score 47; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db |!!!!!!|  
 1 DRVYIHPF 8  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RESULT 2  
 ID Q95J13; PRELIMINARY;  
 PR; 245 AA.  
 DR EMBL; AK018763; BAB31393.1; -.  
 DT 01-DEC-2001 (TREMBIrel. 19, Created)  
 DR 01-DEC-2001 (TREMBIrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBIrel. 19, Last annotation update)  
 DE ANGiotensinogen (FRAGMENT).  
 GN REN.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Pan.  
 NCBI\_TAXID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=504, AND 505;  
 RA Satta Y.;  
 RT "Comparison of DNA and protein polymorphisms between humans and  
 chimpanzees." to the EMBL/GenBank/DDBJ databases.  
 DR Submitted (MAY-2001) to the EMBL; AB062028; BAB5856.1; -.  
 DR EMBL; AB062028; BAB5857.1; -.  
 FT NON\_TER 245 245  
 SQ SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match 100.0%; Score 47; DB 6; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 0.31; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 |||||||  
 Db 34 DRVYIHPF 41

RESULT 3  
 ID Q9D2V0 PRELIMINARY;  
 AC Q9D2V0 PRT; 461 AA.  
 DT 01-JUN-2001 (TREMBIrel. 17, Created)  
 DT 01-JUN-2001 (TREMBIrel. 17, Last sequence update)  
 DE ANGiotensinogen.  
 GN AGT.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7Bl/6J; TISSUE=CEREBELLUM;  
 RX MEDLINE=21035660; PUBMED=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T.,  
 RA Rieplscimann W., Gaasterland T., Gissi C., King B., Kochina H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido R., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiva M., Lee N.H.,  
 RA Lyons P., Marchionni L., Masilima J., Mazzarelli J., Mombretti P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.-H., Weltz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,

RESULT 4  
 ID Q96FD5 PRELIMINARY;  
 AC Q96FD5 PRT; 477 AA.  
 DT 01-DEC-2001 (TREMBIrel. 19, Created)  
 DT 01-DEC-2001 (TREMBIrel. 19, Last sequence update)  
 DE SIMILAR TO ANGiotensinogen.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Strubisberg R.;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC011231; AAH1231.1; -.  
 SQ SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;  
 RA Strubisberg R.;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC011231; AAH1231.1; -.  
 SQ SEQUENCE 477 AA; 51985 MW; AB7988B70592FDE2 CRC64;

Query Match 100.0%; Score 47; DB 4; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 0.42; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
 |||||||  
 Db 25 DRVYIHPF 32

RESULT 5  
 ID Q96F91 PRELIMINARY;  
 AC Q96F91 PRT; 485 AA.  
 DT 01-DEC-2001 (TREMBIrel. 19, Created)  
 DT 01-DEC-2001 (TREMBIrel. 19, Last sequence update)  
 DE ANGiotensinogen (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE A (ALPHA-1 ANTI-PROTEINASE, ANTITRYPSIN), MEMBER 8).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;  
 RA Strubisberg R.;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC011519; AAH11519.1; -.  
 SQ SEQUENCE 485 AA; 53114 MW; 50BA5E9DCD4C8E7F CRC64;

Query Match 100.0%; Score 47; DB 4; Length 485;  
Best Local Similarity 100.0%; Pred. No. 0.43; 0; Mismatches  
Matches 8; Conservative 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
||| | | | |  
Db 34 DRVYIHPF 41

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RESULT 6  
Q9CIP7 PRELIMINARY; PRT; 485 AA.  
ID Q9CIP7; Q9CIP7; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
AC Q9CIP7; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
ID Q9CIP7; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
AC Q9CIP7; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOGENIN.

GN ACT.  
OS Pan troglodytes (Chimpanzee); Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Pan.  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shattuck-Bidens D.; McGrail M.; Stone S.; Mcgrail M.'; Stone S.;  
RT "Germline mutations in the angiotensinogen gene cause predisposition  
to type 1 diabetes mellitus";  
RL Submitted (SERP-1999) to the EMBL/GenBank/DDBJ databases.  
CC -1 SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF108487; AAC29056; 1;  
DR IPR000227; Angiotensinogen.  
DR InterPro; IPR000215; Serpin.  
DR PRINTS; PRO0654; ANGIOGENIN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW SERPIN; PS00284; SERPIN; 1.  
SQ SEQUENCE 485 AA; 53140 MW; 49EBB54AF31F8ADC CRC64;

Query Match 100.0%; Score 47; DB 6; Length 485;  
Best Local Similarity 100.0%; Pred. No. 0.43; 0; Mismatches  
Matches 8; Conservative 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
||| | | | |  
Db 34 DRVYIHPF 41

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RESULT 7  
Q9GPB6 PRELIMINARY; PRT; 485 AA.  
ID Q9GPB6; Q9GPB6; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
AC Q9GPB6; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
ID Q9GPB6; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
AC Q9GPB6; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOGENIN.

GN Gorilla gorilla (gorilla).  
OS Gorilla gorilla (gorilla).  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
NCBI\_TaxID=9593;  
RN [1]  
SEQUENCE FROM N.A.  
RA Shattuck-Bidens D.; McGrail M.; Stone S.;  
RT "Germline mutations in the angiotensinogen gene cause predisposition  
to type 1 diabetes mellitus";  
RL Submitted (SERP-1999) to the EMBL/GenBank/DDBJ databases.  
CC -1 SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF108488; AAC29057; 1;  
DR InterPro; IPR000227; Angiotensinogen.  
DR PRINTS; PRO0654; ANGIOGENIN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW SERPIN; PS00284; SERPIN; 1.  
SQ SEQUENCE 485 AA; 53110 MW; C14C67E49A53F05F CRC64;

Query Match 100.0%; Score 47; DB 6; Length 485;  
Best Local Similarity 100.0%; Pred. No. 0.43; 0; Mismatches  
Matches 8; Conservative 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8  
||| | | | |  
Db 34 DRVYIHPF 41

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RESULT 9  
Q9TSZ0 PRELIMINARY; PRT; 486 AA.  
ID Q9TSZ0; Q9TSZ0; 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
AC Q9TSZ0; 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
ID Q9TSZ0; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
AC Q9TSZ0; 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOGENIN.

GN ANGT.  
OS Callithrix jacchus (Common marmoset);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
NCBI\_TaxID=9483;  
RN [1]  
SEQUENCE FROM N.A.

RX MEDLINE=20065005; PubMed=10598135;  
 RA Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;  
 RT "Cloning and characterization of marmoset renin: comparison with human  
 renin";  
 RL J. Cardiovasc. Pharmacol. 34:893-897(1999).  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; AJ132343; CAB64880.1; --.  
 DR InterPro; IPR000227; angiogenesn.  
 DR InterPro; IPR002125; Serpin.  
 DR Pfam; PF00079; serpin\_1.  
 DR PRIMIS; PR00654; ANGIOGENESN.  
 DR SMART; SM0093; SERPIN\_1.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Serpin; Signal; --.  
 FT SIGNAL 1 33 POTENTIAL.  
 CHAIN 34 486 AA; 53374 MW; 54081292F71F8B CRC64;  
 SQ SEQUENCE 486 AA; F2BD3E53E0ED21F0 CRC64;

Query Match 100.0%; Score 47; DB 6; Length 486;  
 Best Local Similarity 100.0%; Pred No. 0.43; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYVHFF 8  
 DB 34 DRVYVHFF 41

RESULT 10  
 OPS07 PRELIMINARY; PRT; 10 AA.  
 ID OPS07; AC Q9PS07; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE ANGOTENSI T, ANG I.  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 RN [1] NCBI\_TAXID=8496;  
 RP SEQUENCE.  
 RX MEDLINE=93307610; PubMed=8319878;  
 RA Takei Y., Sildorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
 Stephens G.A., Sakakibara S., New angiotensin I isolated from a reptile, Alligator mississippiensis \*, Gen. Comp. Endocrinol. 90:214-219(1993).  
 RA TATEI Y., SILDORFF E.P., HASEGAWA Y., WATANABE T.X., NAKAJIMA K., STEPHENS G.A., SAKAKIBARA S., NEW ANGIOTENSIN I ISOLATED FROM A REPTILE, ALLIGATOR MISSISSIPPIENSIS \*, GEN. COMP. ENDOCRINOL. 90:214-219(1993).  
 RT [1]  
 RL SEQUENCE. 10 AA; CEE38D0761F2DB42 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 10;  
 Best Local Similarity 87.5%; Pred No. 0.012; 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYVHFF 8  
 DB 1 DRVYVHFF 8

RESULT 11  
 Q9HA44 PRELIMINARY; PRT; 295 AA.  
 ID Q9HA44; AC Q9HA44; DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE CDNA FLJ12268 FLS, CLONE MAMMAL01627, HIGHLY SIMILAR TO HOMO SAPIENS TRANSCRIPTION FACTOR TBX6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RX NCBI\_TAXID=9606;

RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY GLAND;  
 RA Isojiri T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H., Nagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murkami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Nitomiya K., Iwayanagi T., NEDO human cDNA sequencing project \*, Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK022330; BAB14014.1; --.  
 DR HSSP; P24781; IXBR.  
 DR InterPro; IPR001699; T-box.  
 DR Pfam; PF00907; T-box.  
 DR PRINTS; PR0093; Tbox.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01264; TBOX; 2; 1.  
 DR PROSITE; PS50252; TBOX; 3; 1.  
 DR SEQUENCE; 295 AA; 33197 MW; F2BD3E53E0ED21F0 CRC64;

Query Match 87.2%; Score 41; DB 4; Length 295;  
 Best Local Similarity 100.0%; Pred No. 3.8; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYVHFF 7  
 DB 170 DRVYVHFF 176

RESULT 12  
 Q9KIA7 PRELIMINARY; PRT; 128 AA.  
 ID Q9KIA7; AC Q9KIA7; DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE HYPOTHETICAL PROTEIN NMB0260.  
 GN NMB0260.  
 OS Neisseria meningitidis (serogroup B);  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 RX NCBI\_TAXID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRATUM=MC58 / SEROGROUP B;  
 RX MEDLINE=20175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Pedersen J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Yamane J., Gill J., Scarlato V., Moxon R., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappoli R., Venter J.C., Science 287:1809-1815(2000).  
 RA "Complete genome sequence of Neisseria meningitidis serogroup B strain DR TIGR; NMB0260; AF40714.1; --.  
 DR TIGR; NMB0260; AF40714.1; --.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 128 AA; 14407 MW; AFFFD965B79ECFC6 CRC64;

Query Match 85.1%; Score 40; DB 16; Length 128;  
 Best Local Similarity 62.5%; Pred No. 2.5; 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYVHFF 8  
 DB 23 DRVYVHFF 30

RESULT	13	RP	SEQUENCE FROM N.A.
Q9PG09	PRELIMINARY;	PRB;	132 AA.
ID Q9PG09;			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE HYPOTHETICAL PROTEIN XFO493.			
GN XFO493.			
OS <i>Xylella fastidiosa</i> .			
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;			
OC <i>Xylella</i> .			
OX NCBI_TAXID=3371;			
RN [1]			
RP STRAIN=9A5C;			
RC SEQUENCE FROM N.A.			
RX MEDLINE=20365717; PubMed=10910347;			
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Accencio M., Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista-C.S., Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Coutinho L.I., Cristofani M., Dias-Meto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Garnier M., Goldman G.H., Goldman H.H.S., Gomes S.L., Gruber A., Ho P.L., Homaisel J.D., Junqueira M.I., Kembel E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lamas M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopez C.R., Machado J.A., Machado M.A., Madrins E.A.L., Martins E.M.F., Madeira H.M.F., Martin C.L., Merck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimiento A.L.T.O., Netto L.E.S., Nanni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Pergolino R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshahko M.H., Valdella H., Van Sluys M.A., Verjovsk-Almeida S., Vettore A.L., Zago M.A., Zatz M., Medanis J., Setubal J.C.; RT "the genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ."; RL Nature 406:151-155(2000); EMBL: AB00388; AAC83303.1; KW Hypothetical protein; complete proteome.			
SQ SEQUENCE 132 AA; 14458 MW; B69EFEC9915E1F CRC64;			
Query Match 85.1%; Score 40; DB 16; Length 132; Best Local Similarity 62.5%; Pred. No. 2,6; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	RESULT	15	RP STRAIN=JCM 1045 / 7;
QY 1 DRVYTHPF 8	ID	048244	RX PubMed=11572479;
Db 91 DRIVHVPF 98	ID	048244	RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoya A., Fukui S., Nagai Y., Nishi-Jima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A., RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A., RA Oshima T., Kikuchi H.;
	AC	048244;	RT "Complete genome sequence of an aerobic thermoacidophilic archaeon, <i>Sulfolobus tokodaii</i> strain7.,"
	DR	DR DNA Res. 8:123-140(2001).	
	DR	DR EMBL: AP000986; BAB6458.1; "-" protein;	
	KW	KW Hypothetical protein; Complete proteome;	
	SQ	SQ SEQUENCE 171 AA; 18700 MW; 897F397AD34EF0A CRC64;	
Query Match 78.7%; Score 37; DB 8; Length 168; Best Local Similarity 62.5%; Pred. No. 13; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	QY 1 DRVYHPP 8	QY 1 DRVYTHPF 7	QY 1 DRVYTHPF 7
RN [1]			

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Db 113 |:||| 11:  
113 DKVYFHPY 120

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Job time: 217 sec